

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 117210

TO: Robert Landsman Location: rem/4d83/4c70

Art Unit: 1647

Wednesday, March 24, 2004

Case Serial Number: 09/646224

From: Peggy Ruppel

Location: Biotech-Chem Library Phone: 571-272-2557

**REM E01b65** 

peggy.ruppel@uspto.gov

## Search Notes

Dear Examiner Landsman:

The results for your search request are attached.

Feel free to contact me if you have any questions.

Thank you for using STIC services.

Peggy Ruppel 2-2557

BEST AVAILABLE COPY



thanks

Robert Landsman, Ph.D **Patent Examiner** Remsen, Rm 4D83, AU 1647 571.272.0888 U.S. Patent and Trademark Office robert.landsman@uspto.gov

Searcher: Phone:\_ Location: Date Picked Up: Date Completed: Searcher Prep/Review: Clerical: Online time:\_

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (wh	ere applic.)
STN:	
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RESULT 2 US-09-354-147C-41 VS-09-364-147C-41 Sequence 41, Application US/09354147C Patent No. 6573067

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RESULT 3
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APPLICANT: Dib-Hajj,
APPLICANT: Waxman,
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
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PRIOR FILING DATE: 1998-11-20
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PRIOR FILING DATE: 198-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
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PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
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NUMBER OF SEQ ID NOS: 44
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
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APPLICANT: Waxman,
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LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence
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ORGANISM: Homo
                                                                                                                       LOCATION: (19)..(5313)
NAME/KEY: unsure
LOCATION: (5804)
                                                                                                         OTHER INFORMATION: cDNA sequence of mouse NaN, n =
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ORGANISM: Mus musculus
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Score 47.4; DB 4;
Pred. No. 2.2e-06;
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Best Local S
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CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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APPLICANT: Waxman, Stephen G
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS:
LOCATION: (41)..(5335)
LOCATION: (19)..(5335)
OTHER INFORMATION: cDNA sequence for rat NaN
NAME/KEY: unsure
LOCATION: (1996)..(4042)
OTHER INFORMATION: n = a or c or g or t. Xa
OTHER INFORMATION: 652 is Leu; Xaa at amino
OTHER INFORMATION: or Lys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCAGCGATTTTTCGTACCAACG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 140
                                                                                                                                                                                                                                                                                          TTAGAAATTTACAGAAAACAGTTTCCCCCCAAAAGCAACCAGATCGATGCTTTCCCAAGG 3019
                                                                                                                                                                                                                                                       201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.8; DB 4;
Pred. No. 7.7e-06;
0; Mismatches 47
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Wehrman,

, Feiyan n, Rui-hong Qing A.

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25).
US-09-620-312D-348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 736, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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SEQ ID NO 348
LENGTH: 4062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT
                 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.

COMPUTER: HP Vectra 486/33

COPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5256 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 CGCTTTTAGGAAATAGCCACAGATGTCTAATGTGACCAGTTGATT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATAATTTGGAACTGGGTAAACATCAAGTTGAACAAGTTCATTAGAAGAGGCATAGAG 448
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                                                                                                                                                                 CITY: Rockville
STATE: Maryland
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                      STREET: 9410 Key West Avenue
APPLICATION NUMBER: US/08/956,171E
                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                     Patrick S. Dillon
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                                                                                         3.50 inch, 1.4Mb storage
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RESULT 7
US-08-161-286-2
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                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: WOO, SAVIO L. C.
APPLICANT: NORDLOH, PETER W.
APPLICANT: STENLUND, ARNE
TITLE OF INVENTION: EPISOMAL
TITLE OF INVENTION: THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08161286 Patent No. 5674703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 736:
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  STREET: 611 ...
CITY: Los Angeles
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: 9B248P1
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: FILING DATE: 02 DE
                                                                                               CLASSIFICATION:
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 780 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 TAATCCTGTAATCAGCAAATCAGTCATAACATTGATACTGTCAGAATGTGATGCTTTCGG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 ATAATAACTGCCCGTATCGTATAAATGAATCGGTTCTAAGTTAAATGCACCTGAACGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 TTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGA 126
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                                                                                                                                                                                                                                                                                                                                           611 West Sixth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                         WOO, SAVIO L. C.
NORDLOH, PETER W.
STENLUND, ARNE
VENTION: EPISOMAL VECTORS
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02 DECEMBER 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%;
                 : including application
: described below:
  07/984,400
                                                                                                                                 US/08/161,286
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Pred. No. 0.
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504

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:

204/252

Warburg, Richard J

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US-08-851-843A-68
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrews, William H.

IITLE OF INVENTION: No. 6093809el Telomerase

UMBER OF SEQUENCES: 225
                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213)
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                                                           FILING DATE: 0
CLASSIFICATION:
                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
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                                                                        APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
NAME: Apple, Rando
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1244 ACTATCAGAATATTGAATTAACCTTTATTAATGCTTTAAAGCTCTGGCTAAAAGGAA 1303
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Two Embarcadero Center, 8th Floor
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ilarity 57.4%;
Conservative
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Harley, Calvin
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Chapman, Karen B.
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Pred. No. 1.2;
0; Mismatches
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RESULT 9
US-08-974-549A-111
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                                                                                           SOFTMARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 111, Application US/08974549A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTAL.

ZIP: 9411-385-
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OFFICE PC-DOS/MS-DOS
COMPUTER: OFFICE PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Andrews, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                 FILING DATE: 18-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IOCATION: join(959..1216, 1273..1353, 1425..1543, IOCATION: 1595..1857, 1894..2286, 2326..2396, 2433...2705, IOCATION: 2746..2862, 2914..3083, 3125..3399, 3356..3504, IOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..4392, IOCATION: 4435..4597, OTHER INFORMATION: telomerase catalytic subunit (TRT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0300
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/ENTION: Human Telomerase Catalytic Subunit
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US 08/846,017
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APPLICATION NUMBER:

FILING DATE:

25-APR-1997

DATA:

FILING DATE:

06-MAY-1997

US 08/851,843

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                                                                                                                                                                                           Sequence 68, Application US/08854050 Patent No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 5544 base pair
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NAME: Apple, Randolph Te
REGISTRATION NUMBER: 36,
                                                                                                                               APPLICANT:
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                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 58; Conserv
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LOCATION:
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REFERENCE/DOCKET NUMBER: 015389-002610US
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nucleic acid
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                                                                                                                                                                                                                                                                                              TGACACATCAGGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAA 4468
                                                                                                                                                                                                                                                                                                                            TGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAA 168
                                                                                                                                                                                                                                                                                                                                                                                         CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
                                                                                                          Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                              Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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14-AUG-1997
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14-AUG-1997
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RESULT 11 US-09-430-323-68

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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UI
FILING DATE: 01-OCT-1:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 18-APR-
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                               LOCATION:
LOCATION:
LOCATION:
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                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph
REGISTRATION NUMBER: 30
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                               OCATION:
4424
                                                                    4364 CGTTTCTTGTCCTCTGCAGAAGTCAAATGGTACGTGTCGGTCTCGAGACTTCAGCAATAT
                                 124 TGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAA 168
                                                                                                   64 CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
                                                                                                                                        58;
                                                                                                                                                          Similarity
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California
TGACACATCAGGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAA 4468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                            join(959.1216, 1273.1353, 1425.1543, 1595.1587, 1894.2286, 2326.2396, 2436.2705, 2746.2862, 2914.3083, 3125.3309, 3356.3504, 3546.3759, 3797.4046, 4086.4252, 4296.4392, 4435.4597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                        13.9%;
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                                                                                                                                                                                                                              telomerase
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                                                                                                                                                                                                                            note= "Schizosaccharomyces pombe"
| note= "Schizosaccharomyces pombe:
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                                                                                                                                      ; Score 29.8; Di
; Pred. No. 2.6;
0; Mismatches
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                                                                                                                                                                       Length 5544;
                                                                                                                                          Indels
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                                                                     4423
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GENERAL INFORMATION: APPLICANT: Cech

ch, Thomas R. ngner, Joachim

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TELEPAX: (415) 576-0200

OTHER INFORMATION: /note= "Schizosaccharomyces pombe telomerase catalytic subunit (TRT)"

SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-430-323-68
                                                                                                                                                                     RESULT 12
US-08-912-951-111
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                                                                                                                                   Sequence 111, Application US/08912951 Patent No. 6475789
                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                               GENERAL INFORMATION:
                                                         APPLICANT:
                                                                                           APPLICANT:
                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/854,050
PILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
PILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
PILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
PILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
PILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/430,323
FILING DATE: 29-Oct-1999
                                                                                                                                                                                                                                                                                                                               4364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
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                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                       CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                     TGACACATCAGGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAA 4468
                                                                                                                                                                                                                                                                                     TGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAA 168
                                                                                                                                                                                                                                                                                                                               CGTTTCTTGTCCTCTGCAGAAGTCAAATGGTACGTGTCGGTCTCGAGACTTCAGCAATAT 4423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                             Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Morin, Gregg B.
Harley, Calvin
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5544;
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                                                                           Matches
                                                                                                                Query Match
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                                                                                                Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 5544 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
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NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

Townsend and Townsend and Crew LLP

ADDRESSEE: Townsend and Townsend and Crew LLP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-APR-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 25-APR-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 06-MAY-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              LOCATION: join(959..1216, 1273..1353, 1425..1543, LOCATION: 1595..1857, 1894..2286, 2326..3396, 2436..2705, LOCATION: 2746..2862, 2914..3083, 3125..3309, 3356..3504, LOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..4392, LOCATION: 4435..4597)
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                                                                                                                                                                         LOCATION: 3546..3759, 3797..4046, 4086..4252, 4296..431
LOCATION: 4435..4597)
OTHER INFORMATION: /note= "Schizosaccharomyces pombe
OTHER INFORMATION: telomerase catalytic subunit (TRT)"
                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
  4364 CGTTTCTTGTCCTCTGCAGAAGTCAAATGGTACGTGTCGGTCTCGAGACTTCAGCAATAT 4423
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California
                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                              Similarity
                                  CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
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25-APR-1997
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                                                                                              13.9%;
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                                                                           Score 29.8; D
Pred. No. 2.6;
0; Mismatches
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                                                                                                                DB 4;
                                                                                                                    Length 5544;
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RESULT 13
US-09-402-181B-111
; GENERAL INFORMATION:
APPLICANT: Cech,
Ling;
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                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 111: US-09-402-181B-111
                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                      Matches
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Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-OCT-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
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                                         4364
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                                                                                                                      58;
TGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAA 168
                                       CGTTTCTTGTCCTCTGCAGAAGTCAAATGGTACGTGTCGGTCTCGAGACTTCAGCAATAT 4423
                                                                  CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACACATCAGGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAA 4468
                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Schizosaccharomyces pombe telomerase catalytic subunit (TRT)"
                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
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                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300
OTHER INFORMATION: /noi
                                                                                                                                                                                                                                                                                                                                                                               NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'ILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICATION NUMBER: US 08/846,017
                                                                                                                    Conservative
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Chapman, Karen B.
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                                                                                                                                    13.9%;
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                                                                                                                    0,
                                                                                                                                      Score 29.8; D
Pred. No. 2.6;
                                                                                                                    Mismatches
                                                                                                                                                         DB 4;
                                                                                                                    47;
                                                                                                                                                           Length 5544;
                                                                                                                    Indels
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                                                                                                                  Gaps
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; telomerase catalytic subunit (TRT) sequence DESCRIPTION: SEQ ID NO: 111:
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US-09-721-456-111
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                                                                       Best
                                                      Matches
                                                                                      Query Match
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                                                                       Local
                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                       FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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64 CTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCAT 123
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                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/974,549F
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 0
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/724,643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
                                                                                                                                                                                                                                                                                        Apple, Randolph
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                                                                                                                                                                                                                      (415) 576-0200
                                                                       13.9%;
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                                                    pred. No. 2.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/851,843
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                                                                                        Length 5544;
                                                        Indels
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GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 516

LENGTH: 1656

TYPE: DNA

ORGANISM: M.catarrhalis

US-09-540-236-516
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US-09-540-236-516
; Sequence 516, Application US/09540236
; Patent No. 6673910
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Search completed: March 22, 2004, 23:17:31 Job time: 35.3051 secs
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                                                                                                          1423 TTAAAAA 1429
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Minimum DB
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Maximum Match 100%
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is derived by analysis of the total score distribution.
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seq length: 2000000000
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10.3 5875

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9.2 119211

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8.8 1764

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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1749
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US-09-354-147C-41
US-09-354-147C-1
US-09-354-147C-1
US-09-543-147C-1
US-09-543-990A-1
US-09-543-681A-3259
US-09-543-681A-3259
US-09-543-681A-3259
US-09-543-681A-3259
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US-09-338-671-3
US-08-481-190-14
PCT-US93-00869-14
US-08-961-S27-146
US-08-961-S27-126
US-08-961-S27-220
US-08-961-S27-220
US-08-723-306-6
PCT-US96-10041-6
US-09-621-976-3857
US-08-956-10041-5
PCT-US96-100899-17
US-08-956-10041-5
PCT-US93-00869-17
US-08-956-10041-5
PCT-US93-00889-17
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PCT-US93-00889-17
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                                 Sequence 6, Appli
Sequence 41, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 14, Appl
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		Query M Best Lo Matches	NAME/K LOCATI OTHER OTHER 09-354-	ORGANISM FEATURE: NAME/KEY LOCATION COTHER IN	LENGTH:	~10.≪	PRIOR	PRIOR	CURRENT CURRENT	TITLE	GENERAL INI APPLICANT	SULT 1 -09-354- Sequence		4. 4. 4. 17	43	41	ω ω 0 0 0	376	ωω 4+ τυ	3 3 4 3 2 F	30	2 8
103 c 2877 c	46 ] 2817 ]	atc]	NAME/KEY: unsure LOCATION: (922) OTHER INFORMATIO OTHER INFORMATIO OTHER INFORMATIO	g	TH: 3701	, , , , , ,			NT APPI	OF INVENT	GENERAL INFORMATION APPLICANT: Dib-Haj			28.2			•		œ œ	228. 66.		
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GTCCCAGTTTGAAGGAATGAAGGT	TAACTTAATGGAATT            TAACTTAATGGAATT	13 y 88 rvativ	y = c	gene 99)	•	NOS: 44 n Ver. 2	DATE: 1999-0	FILING DATE: 1998-0 APPLICATION NUMBER:	T APPLICATION NUMBER: US	CANT: Waxman, Stepnen G. OF INVENTION: Modulation o	j, Sula	ion US		428 174493	2901 5549	200	176373	2236	1956 2191	1717 1717	516	515
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N H	TAACTTAATGGAATTAGAACCTTCCGGATCTACGAGCACTGAGGCCTC	Score 46.8 Pred. No. 0; Mismatc		human NaN			1-20 PCT/US99/02008 1-29	60/109,4	S/09/354, -16 -0/072.99	n of Sodium -US		54147C	ALIGN	US-09-80	-80-	9	999	889	US-09-71 US-09-03	8 6 6	09-62	09-62
900	CCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT 	6.8; DB lo. 6.8e- natches	t ami	CDNA sec			08	Ñ (	147C	um Channels			ALIGNMENTS	1-9/6-3 4-471A-	312-1 171E-	026-001A-5	8-155-17	-234-163-11 -901-379-11	5-858-1 9-555B-1	515 <i>‡</i> 865-	1-976-	1-976-
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RESULT 2
US-09-354-147C-41
; Sequence 41, Application US/09354147C
; Patent No. 6573067

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RESULT 3
US-09-354-147C-4
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APPLICANT: Dib-Hajj,
APPLICANT: Waxman,
                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILLING DATE: 1999-07-16
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                                               Query Match
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(5313)
NAME/KEY: unsure
LOCATION: (5804)
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5860
TYPE: DNA
ORGANISM: Homo
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PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (31)...(5403)
OTHER INFORMATION: full length cDNA sequence
                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                         OTHER INFORMATION: cDNA sequence of mouse NaN, n = a
                                                                                                                                                                                                                                                               ENGTH: 5822
/ Match 10.3%;
Local Similarity 80.6%;
les 54; Conservative
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Local Similarity 88.1%;
es 74; Conservation
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o. 6573067
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Pred. No. 0.05
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Pred. No. 8.6e-06;
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                                                                                                                                                         Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Pleischmann et al.
APPLICANT: Pleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: CDNA seque
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PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (1996). (4042)
OTHER INFORMATION: n = a or c
OTHER INFORMATION: 652 is Leu;
OTHER INFORMATION: or Lys.
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                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                120 TGAAGGT 126
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                                                 CITY: Rockville
                                  STATE: MD
                 COUNTRY:
ZIP: 20850
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ON: cDNA sequence for rat NaN
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Pred. No. 0.053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09643990A Patent No. 6528289
GENERAL INFORMATION:
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Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/643,990
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NAME: Michelle S. Marke
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186F3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ACATTC 132
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                                                                                                                                                                                         STATE: MD
                                                                                                                                                                                                           CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCAAATTTCCGATAATTGAGGCACCTCTTTCGCTTTCCAATTTAAGAAAATTCGTTGT 64630
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                 APPLICATION NUMBER: US/09/643,990A
                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                      J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                               Hamilton O. Smith
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Pred. No. 2;
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                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1710
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARFITILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 1710
LENGTH: 1632
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Best Local
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Best Local S
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CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64631 TCTTGC 64636
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                 134 GCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 ACATTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
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                                                                                                                                                                                                                    Similarity
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TYPE: nucleic acid
STRANDEDNESS: double
                               TGGGCTGAGAT 204
                                                               TTAGCATTCGGCTTGGATGCTGAATTAAAATCAAACTTTGTAAATGGCGACAGTCTTTTT
TTAGTTTAGAT 1410
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                                                                                                                                                                                                  9.2%;
ilarity 52.7%;
Conservative
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Pred. No. 0.68
0; Mismatches
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Pred. No. 2;
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US-09-543-681A-3259
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                                                                                                                                           US-09-543-681A-3259
                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 3259
                                                                                                                                                                                                                                                                                                                                                                  Sequence 3259, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/09596002
Patent No. 6632636
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Best Local Similarity
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LENGTH: 119211
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OTHER INFORMATION: Incyte template ID No. 6632636 40
PUBLICATION INFORMATION:
-09-596-002-40
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILLING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                        LENGTH: 1095
TYPE: DNA
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                            Local 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 GCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGAAAAGACCAACAGTTCTTTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 TCTACGAGCACTGAGGCCTCTCGTGCGCTGTCCCAGTTTGAAGGAATGAAGGTACATTCT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                      Similarity
                               GCGCTGTCCCAGTTTGAAGGAATGAAGGTACATTCTGCAGAAGAATGGGTAGAAGTTCAG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAGTTTAGAT 109446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patterson,
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Pred. No. 5.6;
0; Mismatches
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                                                                                    Score 31.6; DB 4; Pred. No. 0.65;
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                                                                   Gaps
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 906
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Patent No. 6503729
TITLE OF INVENTION:
FILE REFERENCE: PB275

jannaschii

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon,

Methanococc

CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428

SOFTWARE:

ENGTH:

1664976

TYPE: DNA ORGANISM: Methanococcus jannaschii

NUMBER OF SEQ ID NOS:

PatentIn

PRIOR FILING DATE:

1996-08-22

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                                                                   RESULT 11
US-08-916-421B-1/c
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
sequence 1, Application US/08916421B Patent No. 6503729 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of a region of the major surface TITLE OF INVENTION: 91/coprotein (MSG) gene of human Pneumocystis of FILE REFERENCE: 4239-58054
CURRENT APPLICATION NUMBER: US/09/762,724
CURRENT FILING DATE: 2001-02-09
CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: PCT/US99/18750
PRIOR FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/096,805 PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pneumocystis carinii sp.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                      1795 AGAAAATGCCATAAATGGTCTAGAAGGGGTGATGATCGTTTTTCTTTTGTATGTGTTTTC
                                                                                                                                                                                            268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 TTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTCCTTAAATTGC 217
                                                                                                                                                                                                                                                                             208 CTTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAATTTGAG 267
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                                                                                                                                                                                            GGGTAGAGAAAAGCCTAAGATATACTTTCTACCCTAAAA 306
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NAME/KEY: misc feature LOCATION: (28222)..(28222) OTHER INFORMATION: n equals

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NAME/KEY: misc\_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a
NAME/KEY: misc\_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a
NAME/KEY: misc\_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a
NAME/KEY: misc\_feature

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INFORMATION: n equals  KEY: misc feature  ION: (1602912)(160291	TION: (1470091) R INFORMATION: /KEY: misc_feat TTON: (1569020)	34949 ATION BC fe	(1349473)	: (1313224) FORMATION: n	TION: (1310988) R INFORMATION: n	TION: (1130881) R INFORMATION: n	/KEY: m18C reacur TION: (1119881) R INFORMATION: n	(1096846)	INFORMATION:	TION: (871619)( R INFORMATION: n	TION: (855539)( R INFORMATION: n	(779676)(	(779455)( ORMATION: n	TION: (741684)(	TION: (713652)( R INFORMATION: n	ION: (682442)( INFORMATION: n	TION: (674435). R INFORMATION: /KEY: misc feat	TION: (6572 R INFORMATI /KEY: misc_	TION: (657081)(657081 R INFORMATION: n equals /KEY: misc_feature	TION: (622708)( R INFORMATION: n /KEY: misc_featur	TION: (600992)( R INFORMATION: n /KEY: misc featur	TION: (559241)( R INFORMATION: n /KEY: misc featur	LOCATION: (559167)(559167). OTHER INFORMATION: n equals a, NAME/KEY: misc feature
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NAME/KEY: misc\_feature LOCATION: (98159). (98159) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (98239). (98239) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (98266). (98266) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature

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LOCATION: (234814) ...(234814) COTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (309398) ...(309398) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (309318) ...(309418) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (312837) ...(312837) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (31293) ...(31293) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (31293) ...(31293) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature LOCATION: (319326) ...(319226) OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature

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LOCATION: (234187)..(234187)
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NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature

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NAME/KBY: misc\_feature OCATION: (231980)..(231980) OTHER INFORMATION: n equals

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; LOCATION: (567)...(1616)
US-09-338-671-3
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                                                                                                                                            Matches
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            SCFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Applicat Patent No. 6194638 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/338,671
CURRENT FILLING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 60/090,416
EARLIER FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Alteration of Hemicellulose TITLE OF INVENTION: Concentration in Plants FILE REFERENCE: 0782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dhugga, Kanwarpal
APPLICANT: Fallis, Patricia Lynne
APPLICANT: Nichols, Scott E.
                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1437358 AATATAGATAATGTCAAAGTTAATGGAATTATTGACTTGCAGAACTACTTTGAATTGAAA 1437299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1437298 AACATGGTTGTTGCTAAGTTGGTTACAAATCTGCTTTATATAGAAAGGAGAGTAGA 1437239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 9.0%;
Local Similarity 48.1%;
nes 88; Conservative
1766
                                                                                                 160 AACAGAGAAAGGTGGAAAAGACCAACAGTTCTTTTTGGGCTGAGATTTCCTTAAATTTGCCA 219
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AGCATCTCATTGTATAC 1782
                                   AGCTTTTCCTGGGTTAC 236
                                                                       AACTCATGAAGCTGAAATAAACAACAGTCCTTTATGCCGTGAATTTGGCATGAATAGCTG 1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09338671
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nilarity 62.3%;
Conservative
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Pred. No. 1.9;
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RESULT 13

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PCT-US93-00869-14
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Matches
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                                                                                                                                                                                                                                    Sequence 14, Application PC/TUS9300869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1764 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 203,533
APPLICATION UNMBER: 203,533
APTORNEY, AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: UA 8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                         TITLE OF INVENTION: Polypness.
TITLE OF INVENTION: and Applications
TITLE OF GROTIENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: John C. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy
COMPUTER: Macintosh
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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TOPOLOGY: lir
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OPERATING SYSTEM:
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Local Similarity 53.3%;
                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                    ZIP:
                                                                   COUNTRY:
                                                                                               CITY: Trumbull
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                       177 AMACCTTGACACTGTTGATAGGCGAAATGTTCTTTTAGGGTTAGGAGGTCTTTATGGTGC
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25 Skytop Drive
                                                                                                                  E: Yahwak & Associates
25 Skytop Drive
                                                                   USA
                                                                                                                                                                                                                John C. Steffens
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DN: Polyphenol Oxidase cDNA
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                 disk
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RESULT 15

US-09-621-976-3851
(US-09-621-976-3851)

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; NAME/KEY: CDS

; LOCATION: 129..401

US-09-621-976-3851
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US93-00869-14
Search completed: March 22, 2004, 23:17:46
Job time: 62.1608 secs
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Best Local Similarity 64.2%;
Matches 43; Conservative
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8.8%; Score 30.4; DB 5; Length 1764;
Best Local Similarity 53.3%; Pred. No. 2.1;
Matches 64; Conservative 0; Mismatches 56; Indels 0
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SOFTWARE: Patent.pm
SEQ ID NO 3851
LENGTH: 514
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SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00
PILING DATE: 19930129
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (203)268-1951
TELEPAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1764 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1/77 AAACCTTGACACTGTTGATAGGCGAAATGTTCTTTTAGGGTTAGGAGGTCTTTATGGTGC 236
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                                                                                                                                                                                                                                                                                                                                                                                                             | 129 ATTCTGCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTT 188
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                                                                                                                                                                                82 TCTTTCG 388
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                                                                                                                                                                                                                                                   89 CTTTTTG 195
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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  Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/BackfIles1.seq:*

6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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US-09-354-147C-1
US-09-354-147C-1
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US-09-354-147C-1
US-09-96-994-1
US-09-96-994-1
US-09-976-594-756
US-08-836-325-1
US-08-836-325-1
US-08-836-325-1
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US-08-836-325-1
US-08-836-325-1
US-08-843-417-9
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US-09-527-013-9
US-08-843-417-1
US-09-527-013-7
US-08-669-656A-7
US-08-669-656A-7
US-08-669-656A-7
US-09-624-020B-8
US-09-425-043-8
US-09-425-043-8
US-09-425-043-1
US-09-425-043-1
US-09-425-043-2
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US-09-425-043-2
US-09-425-043-2
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US-09-354-147C-6
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45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29
32.4	37.2	37.2	37.2	37.2	37.2	37.2	37.2	38.6	38.6	38.6	38.6	39.6	39.6	43.8	45	47.4
14.5	16.7	16.7	16.7	16.7	16.7	16.7	16.7	17.3	17.3	17.3	17.3	17.8	17.8	19.6	20.2	21.3
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
841, App	24, Appl	7, Appli	7, Appli	7, Appli	7, Appli	7, Appli	7, Appli	1, Appli	1, Appli	2, Appli	2, Appli	3, Appli	10, Appl	14, Appl	1104, Ap	43, Appl

## ALIGNMENTS

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APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
FIILE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REPERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                     US-09-354-147C-6
                                                                                                                                                                                                                                                                                                                                                                     IENGTH: 3701

TYPE: DNA
ORGANIGN: Homo sapiens
FEATURE:
NAME/KEY: CDS
IOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
NAME/KEY: unsure
IOCATION: (922)
OTHER INFORMATION: y = c or t. Xaa at amino acid pos
OTHER INFORMATION: Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09354147C Patent No. 6573067
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              Matches
  3013
                                                                                                                                                                           2896
                                                                                       2955
                                                                                                                                112
                                                                                                                                                                                                                                                              143;
                                                                                                                                                                                                                     52 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                         CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCCTTTTCCTGGAAAA 171
                                                                                                                                                                         AAGGTGGTGATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT
TTTGGGAAATGCATT-AATGGAACAGACT 3040
                         TTTGGGAAATGCATTCAATGGAACAGACT 200
                                                                                       CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                   48.3%;
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Pred. No. 1.4e-23;
                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                         Length 3701;
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RESULT 3
US-09-354-147C-4
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ORANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
US-09-354-147C-41
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APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT EPILION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
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SEQ ID NO 41
LENGTH: 5860
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                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 4
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                                                                                                                                                                                                      APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
ITILE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
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PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                    PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 44
LOCATION:
                                          NAME/KEY:
                                                                   FEATURE:
                                                                                      TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                     ENGTH: 5822
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                     (19) .. (5313)
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Pred. No. 1.6e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Maxman, Stephen G
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/109,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (5804)
OTHER INFORMATION: cDNA sequence of mouse NaN, n = a or c or 9
                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1996)..(4042)
COTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (41)..(53
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 5875
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3584
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                                                                                                                                                  3467 AAGGTTGTCGTCTACGCCCTGATCAGCGCCATACCTGCCATT-CTCAATGTCTTGCTGGT
                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 TTTGGGAAATGCATTCAATGGAACAGACTTTTAGGAATTT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                         tch 32.6%; al Similarity 78.9%; 112; Conservative
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                                                                           CTGCCTCATTTTCTGGCTCGTATTTTGTATCTTGGGAGTAAATTT--ATTTTCTGGGAAG
                                                                                               CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                AAGGTGGTCGATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT
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                                     TTTGGGAAATGCATTCAATGGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGGAAGATGCATT-AATGGAACAGACATAAATAATAT 3603
 TTTGGAAGGTGCATTAACGGGA 3605
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82.5%;
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Pred. No. 4.3e-16;
                                                                                                                                                                                                                           Score 72.8; DB 4;
Pred. No. 9e-13;
0; Mismatches 27;
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. 9e-13;
27;
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                                                                                                                                                                                                                                                                   Length 5875;
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RESULT 5

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; LOCATION: (1)..(6048)
US-09-634-920-3
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
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TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQTI.

TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME

FILE REFERENCE: 2323-155

CURRENT APPLICATION NUMBER: US/09/634,920

CURRENT FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: 60/190,057

PRIOR APPLICATION NUMBER: 60/190,057

PRIOR FILING DATE: 2000-03-17

PRIOR PILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: 60/147,488

PRIOR FILING DATE: 1999-08-09

PRIOR SECULATION SECULATION NUMBER: 00 SECULATION NUMBER: 2000-08-09

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-09

PRIOR PRIOR PILING DATE: 1999-08-09
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APPLICANT: Keating, Mark
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ORGANISM: Homo sapiens
FEATURE;
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION NUMBER: US/09/514,907A
APPLICATION NUMBER: US/09/514,907A
FILING DATE: 08-Feb-2000
CLASSIFICATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
RECOMPATION NUMBER: US/09/514,907A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD. 656770.

ALI INFORMATION:
APPLICANT: Kenneth B. Stokes
APPLICANT: Kenneth B. Stokes
TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC (
SENSING BY CARDIAC PACEMAKERS)
GENETIC TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No.
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3949 TTTGAGGGCATGAGGGTGGTGGTCAATGCCCTGGTGGGCGCCATCCCGTCCA-TCATGAA
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                                                                                                                                                                                                                                                                                                                                                     STATE: PA
                                                                                                                                                                                                                                                                                                   ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
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Pred. No. 1.3e-07;
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US-09-896-994-1
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Best Local Similarity 68.8%;
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                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/514,907
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4066
                                                                                                                                                                             REGISTRATION NUMBER: 38,534
REPERENCE NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOS E MORIBSETTE
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3949 TTTGAGGGCATGAGGGTGGTGAATGCCCTGGTGGGCGCCATCCCGTCCA-TCATGAA 4007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ken Stokes
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                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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STRANDEDNESS: double
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TELEFAX: (215)
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/896,994 FILING DATE: 02-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Philadelphia
                                                                                         LENGTH: 6048 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6048 bases
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DESCRIPTION: SEQ ID NO: 1:
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Pred. No. 1.3e-07;
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RESULT 9
US-08-836-325-13
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mandel,
APPLICANT: Halegou
APPLICANT: Borden,
                                                                                                                                                                                                                                                             Sequence 13, Application US/08836325 Patent No. 6110672
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SOFTWARE: PERL Program
SEQ ID NO 756
LENGTH: 6348
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Patent No. 6673549
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TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 1719478CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                          APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral
TITLE OF INVENTION: Sodium Cha
TITLE OF INVENTION: X-ray Diff
TITLE OF INVENTION: Drug Desig
TITLE OF INVENTION: Thereof
                                       CORRESPONDENCE ADDRESS:
                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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  1100 New York Ave.,
                                                                                                                                                                                               Halegoua,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                      Mandel, Gail
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68.8%;
                                                                                              Peripheral Nervous System Specific
Sodium Channels, DNA Encoding Therefor, Crystallization,
S-ray Diffraction, Computer Molecular Modeling, Rational
Drug Design, Drug Screening, and Methods of Making and Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.4%;
                                                                              Drug Design,
Thereof
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                                                                                                                                                                                                      Simon
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Pred. No. 1.9e-06
0; Mismatches 20
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Pred. No. 1.3e-07;
GOLDSTEIN & FOX P.L.L.C
N. W., Suite 600
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE: 2-MAY-199
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO
                                                                                                                                                                                   APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral
TITLE OF INVENTION: Sodium Char
TITLE OF INVENTION: X-ray Diffi
TITLE OF INVENTION: X-ray Diffi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mucleic acid
STRANDEDNESS: both
TOPOLOGY: both
OLECTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/3: FILING DATE: 02-NOV-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                             TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                             NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
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STATE:
             COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 09
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                    STATE:
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                                                                                                                                                                              Peripheral Nervous System Specific
Sodium Channels, DNA Encoding Therefor, Crystallization,
Sodium Channels, DNA Encoding Therefor, Crystallizational
X-ray Diffraction, Computer Molecular Modeling, Rational
Drug Design, Drug Screening, and Methods of Making and Using
                                                                                                                                                             Thereof
                                                                                                      KESSLER,
                                                                                                                                             19
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Pred. No. 1.9e-06;
                                                                                       GOLDSTEIN & FOX P.L.L.C
N. W., Suite 600
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MEDIUM TYPE:

Floppy disk

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US-08-836-325-14
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Matches
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Best Local Similarity
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Patent No. 611067
                                                                                                                                                                                                                                                  APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral N
TITLE OF INVENTION: Sodium Chanr
TITLE OF INVENTION: X-ray Diffra
TITLE OF INVENTION: Drug Design,
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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LENGTH: 6404 base pairs
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FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
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APPLICATION NUMBER: US,
FILING DATE: 2-MAY-199
CLASSIFICATION: 514
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STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                    STREET: 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                            COUNTRY: USA
ZIP: 20005-3934
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1100 New York Ave.,
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ilarity 73.4%;
Conservative
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Sodium Channels, DNA Encoding Therefor, Crystallization,
X-ray Diffraction, Computer Molecular Modeling, Rational
Drug Design, Drug Screening, and Methods of Making and Using
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Pred. No. 2e-06;
"" anatches 28;
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N. W., Suite 600
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral N
TITLE OF INVENTION: Sodium Chann
TITLE OF INVENTION: X-ray Diffra
TITLE OF INVENTION: Drug Design,
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/3: FILING DATE: 02-NOV-1994 ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
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                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 09:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/1
PTT.TNG DATE: 02-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/
FILING DATE: 2-MAY-1997
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTT 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                          20005-3934
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                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGTAGTGGTCAACGCACTCATAGGAGCAATCCCTTCCA-TCATGAACGTGCTTCTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3033 base pairs
                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                              Halegoua,
                                                                                                                                                                                                                                                                                                                                                                                               Mandel, Gail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..3033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995
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                                                                                                                                                                                                                                                                                    Peripheral Nervous System Specific Sodium Channels, DNA Encoding Therefor, CryX-ray Diffraction, Computer Molecular Mode. Drug Design, Drug Screening, and Methods o
                                                                                                                                                                                                                                                                                                                                                                                Simon
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US/08/836,325
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Pred. No. 4.5e-06;
0; Mismatches 29;
                                                                                                                                                                                               GOLDSTEIN & FOX P.L.L.C
N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0240002
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                                                                                                                                                                                                                                                                                                                            Crystallization,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

08/482,401

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

02-NOV-1995

PCT/US95/14251

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RESULT 13
US-08-843-417-9
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATIN: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Applic
Patent No. 6184349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/3:
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED EBRIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6452 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                  3: Heller Ehrman White & McAuliffe
525 University Ave
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Delgado,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               both
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72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                             SODIUM CHANNEL alpha-SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-527-013-9
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Patent No. 6479259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415)-324-7041
                                                                       CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,417
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IOPOLOGY:
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Herman, Ronald C
Delgado, Stephen
Fish, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3863 GCCTCATCTTCTGGCTCATCTTCAGCATCATGGGTGTGAACCTC--TTCGCAGGGAAGTT 3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3804 GGTGGTGGTGGATGCCCTGGTGGGCGCCATCCCATCCA-TCATGAATGTCCTCCTCGTCT 3862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 TGGGAAATGCATTCAATGGAAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 GCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTTCCTGGAAAATT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 GGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGTCT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 525 University Ave CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGAGGTGCATCAACTATACC 3942
                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/527,013 FILING DATE: 16-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                    TELEPHONE: (415)-324-7041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) -324-0638
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Rabert, Douglas K
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                  (415)-324-0638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
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Pred. No. 6.7e-06;
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SEQUENCE CHARACTERISTICS:

LENGTH: 5874 base pairs TYPE: nucleic acid STRANDEDNESS: unknown

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                                                                            TELEPHONE: (415) 324-7
TELEPAX: (415) -324-03
TIPONATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
MOLECULE TYPE:
                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                   NAME: Schmonsees, William REGISTRATION NUMBER: 31,796 REFERENCE/DOCKET NUMBER: 28340-P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                               STRANDEDNESS:
                                                             TYPE: nucleic acid
                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                6344 base pairs
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Fish, Linda M
Sangameswaran, Lakshmi
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Pred. No. 6.7e-06;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                      Version
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                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: Dorsal root ganglia
CELL TYPE: Peripheral nerve
3907 CTTCAGCATCATGGGCGTGAACCTCTTCGCCGGGAAATTTTCG 3949
                                                                                           3848 GIGGGCGCCATCCCA-TCATGAACGICCTCCTCGTCTGCCTCATCTTCTGGCTCAT 3906
                                                                                                                                                                                       3788 CTCCGACCGCTGCGGGCTCTGTCTCGATTCGAAGGCATGAGGGTAGTGGTGGATGCCCTC 3847
                                       133 ATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAATTTG 175
                                                                                                                                        73 ATAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGTCTGCCTCATTTTCTGGCTCGT 132
                                                                                                                                                                                                                                    13 CCCCATCTGTTATGGTTTTCCTTTGCTTTTCCATAAGGTGGTGGTCAATGCTCTC 72
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Search completed: March 22, 2004, 23:17:49
Job time: 33.3955 secs

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Result
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       Pred
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US-09-354-147C-41
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RESULT 2 US-09-354-147C-41

Sequence 41, Application US/09354147C Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Soc

of Sodium Channels in Dorsal Root Ganglia

유

Matches

50;

Conservative

Query Match Best Local Similarity

19.3%;

Score 47; DB 4; Length 3701; Pred. No. 2e-06; 0; Mismatches 5; Indels

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RESULT 1 US-09-354- Sequence Sequence Sequence Sequence Facent N GENERAL APPLICA FILE RE CURRENT CURRENT FRIOR A PRIOR A PRIOR F PRIOR A PRIOR F P P PRIOR F P P P P P P P P P P P P P P P P P P P	000 0 0 0	
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-147C-6  10 6, Application US/093  NO. 6573067  INFORMATION: ANT: Dib-Hajj, Sulayman ANT: Maxman, Stephen G OF INVENTION: MODIFICATION NUMBER: US FILING DATE: 1998-01-29 APPLICATION NUMBER: US FILING DATE: 1999-01-29 OF SEQ ID NOS: 44  RE: Patentin Ver. 2.1  NO 6  NO 6  REY: CDS TION: (1). (3699) INFORMATION: partial h KEY: unsure TON: (922) INFORMATION: y = c or INFORMATION: Leu.  1-147C-6	111.9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
Application US/09354147C 1573067 1573067 RRATION: Sulayman Maxman, Stephen G. WENTION: Modulation of S NCE: 44574-5004-01-US INICATION NUMBER: US 60/09/3 INICATION NUMBER: US 60/072 (G DATE: 1998-01-29 (G DATE: 1998-11-20 (G DATE: 1999-01-29 (G DATE: 1998-01-29 (G D	1158 11772 11772 11770 11700 10700 1	
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n Dorsal Root Ganglia	Sequence 4, Appli Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 31413, Appl Sequence 3092, Appl Sequence 11413, App Sequence 116, Appl Sequence 26, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 39, Appli Sequence 701, Appli Sequence 39, Appli	

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FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION UMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-29
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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Best Local :
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SEQ ID NO 41
LENGTH: 5860
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NAME/KEY: CDS
LOCATION: (31)..(540
OTHER INFORMATION: f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                           TELEFAX: (415)-324-0638 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pairs
                                                                                                                                                  NAME: Schmonsees, William REGISTRATION NUMBER: 31,796 REFERENCE/DOCKET NUMBER: 28: TELECOMMUNICATION INFORMATION: TELEPHONE: (415)-324-7041
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
STRANDEDNESS: Unki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3789 GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG 3843
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                                             nucleic acid
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ION: full length cDNA sequence for human NaN
                         unknown
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RESULT 4
US-09-527-013-9
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                                                                         US-09-527-013-9
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GENERAL INFORMATION:
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Matches
                   Best Local Similarity
                                   Query Match
                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/527,013

FILING DATE: 16-Mar-2000

CLASSIFICATION TAME: US/09/527,013

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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Local Similarity 72.0%;
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/843,417
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Herman, Ronald C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 525 Univ
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                            LENGTH: 5874 base pairs
 Conservative
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                   17.0%;
72.0%;
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 Score 41.4; DB 4;
Pred. No. 0.00025;
0; Mismatches 21;
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Pred. No. 0.00025;
0; Mismatches 21;
                                   Length 5874;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Schmonsees, William REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 2834
TELECOMMUNICATION INFORMATION: TELEPHONE: (415)-324-7041
TELEPHONE: (415)-324-7038
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                              Matches
                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pair
                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: 1
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TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                           TISUE TYPE: Dorsal root ganglia
                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6344 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 525 University Ave CITY: Palo Alto
                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                   163
                                                                                                                103
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|2, 6184349
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                                                                                ACAGAGGTGA 94
                                                                                                                CTTCTTCAGGTGGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCC 4162
                                                                                                                                              CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
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Fish, Linda M
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74.3%;
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                                                                                                                                                                                            Score 41.2; DB 3;
Pred. No. 0.00031;
                                                                                                                                                                            Mismatches
                                                                                                                                                                              18;
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Patent No. 6479259
GENERAL INFORMATION:
                                                                                                                                                        Matches
                                                                                                                                                                           Best
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415)-324-0638 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,417
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/527,013
FILING DATE: 16-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
                                                                                                                                                                                                                                                    ORGANISM: rat
TISSUE TYPE: Dorsal root ganglia
CELL TYPE: Peripheral nerve
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                           4103 CTTCTTCAGGTGGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCC 4162
                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Heller Ehrman White & McAuliffe
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4163 GGAGAGATCA 4172
                                    85 ACAGAGGTGA 94
                                                                                                                  25
                                                                                                                                                      l Similarity
52; Conserv
                                                                                                           CTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 6344 base pairs
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                                                                                                                                                      16.9%;
ilarity 74.3%;
Conservative
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Fish, Linda M
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                                                                                                                                                      0
                                                                                                                                                  Score 41.2; DB 4;
Pred. No. 0.00031;
0; Mismatches 18;
                                                                                                                                                        18;
                                                                                                                                                                                             Length 6344;
                                                                                                                                                        Indels
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RESULT 7 US-08-669-656A-1

Sequence 1, Application US/08669656A Patent No. 6451554

GENERAL INFORMATION:

APPLICANT: Wood, John N.

APPLICANT: Akopian, TITLE OF INVENTION: NUMBER OF SEQUENCES:

Armen N.

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: ZENECA Pharmaceuticals
1800 Concord Pike, P.O. Box 15437

STREET: 1800 Cond CITY: Wilmington

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GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656A
FILING DATE: 24-TUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                           APPLICANT: Wood, John N.
APPLICANT: Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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LOCATION:
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                                                                                                                                                                  STREET: 1800 Cond
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IORNBY/AGENT TOTAL D.

NAME: Hohenschutz, Liza D.

REGISTRATION NUMBER: 33,712

REGISTRATION NUMBER: PHM.70086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
   APPLICATION NUMBER:
                                                                                                                                ZIP: 19850
                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                        ADDRESSEE: ZENECA Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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204..6077
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US/08/669,656A
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RESULT 9
US-08-669-656A-5
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; LOCATION:
US-08-669-656A-7
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Best Local Similarity 74.3
52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (302) 886-7
INFORMATION FOR SEQ ID NO:
                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                           SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656A FILING DATE: 24-JUN-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Love
CITY: Wilmington
CTATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, John N.
APPLICANT: Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
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                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,71
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                                               TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                  NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,71 REFERENCE/DOCKET NUMBER: I
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: CDS
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                                                                                                ENGTH:
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                                                                                                7052 base pairs
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1800 Concord Pike, P.O. Box 15437
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ER: PHM.70086
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Pred. No. 0.00031;
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 347316.1
US-09-976-594-1104
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US-09-976-594-1104
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Best Local S
Matches | 54
                                                                                                                                                                                                              Sequence 3, Application US/09634920 Patent No. 6342357 GENERAL INFORMATION:
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SEQ ID NO 1104
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GENERAL INFORMATION:
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                                                    APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG OT SYNDROME GENES KVLQTI AND
TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2323-155
CURRENT FILING DATE: 2000-08-09
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/190,057
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTMARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
Q ID NO 3
LENGTH: 6048
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52; Conserv
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                           PatentIn Ver. 2.0
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ilarity 74.3%;
Conservative
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70.1%;
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Pred. No. 0.00063;
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Pred. No. 0.00033;
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US-09-514-907A-1
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                                                                                                     Matches
                                                                                                                                 Query Match
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Best Local
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LOCATION: (1)..(6048)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                  Local
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ADDRESSEE: Woodcock
STREET: One Liberty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 12
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                85 ACAGAG
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                                                                                                                                                                                                                                                                      TELEPHONE: (215)
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ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
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                  90
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72.7%;
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72.7%;
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Sequence 1, Application US/09514907A Patent No. 6567705
GENERAL INFORMATION:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 6048 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,907A
FILING DATE: 08-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jos, e Morissette
TITLE OF INVENTION: SYSTEMS
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kenneth B. Stokes
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                                CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 38,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEMS FOR ENHANCING CARDIAC SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATMENT
                                                                                                                                                                                                                                                                                           568-3439
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Place - 46th Floor
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Pred. No. 0
                                                                                      Score 37.2; DB 4
Pred. No. 0.0079;
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                                                                       Mismatches
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                                                                                                         DB 4;
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                                                                                                         Length 6048;
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US-09-354-147C-1
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Patent No. 6665563
GENERAL INFORMATION:
Sequence 1, Application US/09354147C
Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.2%;
Best Local Similarity 72.7%;
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-09-896-994-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/514,907
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,994
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Jos e Morissette
                                                                                                                                                                                                                                                                                                            4294 AGGGGG 4299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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US-09-024-020B-1
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GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/024

FILING DATE: 16-FEB-1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039

FILING DATE: 26-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.

REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R002

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1052-3097
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: cDNA sequence for rat NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FISH, LANGE, APPLICANT: FISH, LANGE, C.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n = a or c of OTHER INFORMATION: 652 is Leu; OTHER INFORMATION: or Lys.
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LOCATION: (1996)..(4042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIF: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3401 HII
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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78.2%;
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Pred. No. 0.025;
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Search completed: March Job time : 34.2579 secs	Qy 85 A Db 4291 C	Oy 25 C Db 4231 C	Query Match Best Local Similarity Matches 47; Conser	; TYPE; nu STRANDEDN ; TOPOLOGY: ; MOLECULE TY US-09-024-020B-1
Search completed: March 22, 2004, 23:17:50 Job time : 34.2579 весв	85 ACAGAG 90 	25 CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84	ch 14.6%; Score 35.6; DB 3; Length 5977; 1 Similarity 71.2%; Pred. No. 0.029; 47; Conservative 0; Mismatches 19; Indels 0; Gaps 0;	TYPE: nucleic acid STRANDEDNESS; single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) -024-020B-1

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nucleic search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Title:
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/backfIles1.seq:*

6: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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Sequence 41,
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46, Appli
41, Appli
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3326 TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 3377

Query Ma Best Loo Matches Qy Db Db Qy Qy	FACTURE FILL RAPITOR FILL RAPITOR FILL REPRIOR AFFICE REPRIOR FILE PRIOR FILE	28 29 31 31 31 31 31 31 31 31 31 31 31 31 31
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Similarity 5; CONSERVAT ATTICTAACAGA	Application 6573067 CMARTION: Dib-Hajj, Su Waxman, Ste WAXMAN, Ste NVENTION: Mod ENCE: 44574-5 ENCE: 44574-5 ENCE: 41574-5 ENCE 14574-5 ENCE: 41574-5 ENCE: 41574-5 ENCENTION NUMBE ICATION NUMBE ICAT	บับบันส.ส.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ.ผ
32.9% 90.1% 90.1% AGAAAGAAA	Sulaymai   Stephen (	551133154374 651133154 651133154 631133154
imilarity 90.1%; Pred. No. 6.3e-27; CONSETVATIVE 0; MISMATCHES 1; GAP ATTTCTAACAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT- ATTCCACAGAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT- ATTCCACAGAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTA TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT TTGACAACTTCAACCAGAAAAAGGTTAAGTATCTCGGGTTGTCTTGAT 372 TTGACAACTTCAACCAGACAAAAAGGTTAAGTGGCGAAGAAATTTTTAT 3377	47C  f Sodium Channel  9/354,147C  072,990  109,402  99/02008  99/02008  xaa at amino ac	4 US-09-976-594-756 3 US-08-836-325-14 2 US-08-808-793-26 3 US-07-998-2898-7 2 US-08-808-793-24 2 US-08-808-793-2 2 US-08-98-793-7 2 US-08-793-702-7 1 US-08-338-702-7 1 US-08-338-702-7 2 US-08-338-702-7 2 US-08-338-702-7 3 US-08-724-095-7 5 PCT-US95-14262-7 5 PCT-US95-14262-7 2 US-08-724-095-7 3 US-08-725-14362-7 3 US-08-725-14362-7 3 US-08-772-512A-1
; Gaps ; Gaps CATIT-CT 26 [        CATITACT 32 CGITATCA 32         CGITATCA 33 372	in Dorsal	Sequence 756, Appl Sequence 13, Appl Sequence 24, Appl Sequence 3, Appli Sequence 24, Appli Sequence 24, Appli Sequence 2, Appli Sequence 7, Appli Sequence 1, Appli Sequence 20, Appli Sequence 20, Appli
1; 0 65 0 0		

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APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR PILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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APPLICANT: Dib-Hajj,
APPLICANT: Waxman,
                                                                                                                             SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09354147C Patent No. 6573067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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TYPE: DNA
ORGANISM: Homo s
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                             TYPE: DNA ORGANISM: Mus musculus
                  NAME/KEY: CDS
                                           FEATURE:
                                                                                                           ENGTH: 5822
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(19) .. (5313)
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Pred. No. 7.4e-27;
D; Mismatches 16
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NAME/KEY: Unsure

LOCATION: (1996)..(4042)

OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.

US-09-354-147C-1
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                                                                                                                                                                                                                                 Best Local
Matches 12
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SOFTWARE: PatentIn Ver
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09354147C Patent No. 6573067
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                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: cDNA sequence for rat NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 5875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
3903
                                                                                                                                                         3783 ATTCCAGAGAGAAAGACGAGCAGCCGGACTTTGAGGCGAACCTCTACGCGTATCTCTACT
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                                                                                                                  261
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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                                    TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                             TTGTGGTTTTTATCATCTTCGGCTCCTTCTTTACCCTGAACCTCTTTATCGGTGTTATTA
                                                                                                      TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                  ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGA-GAGCAATTCACTCGGTTACATTTCT
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  TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT
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70.9%;
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Pred. No. 2.6e-14;
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Pred. No. 1.4e-12;
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                                                                                                                                                                                                                                         49;
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RESULT 5

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                                                                                                                                  US-09-425-043-1
                                                                                                                                                    RESULT 6
                                                                                          Sequence
Patent No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 852-3097
TELEPAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5977 base pairs
TYPE: nucleic acid
GTP NETRUESC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/039,447
PILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: RCTELECOMMUNICATION INFORMATION:
                                      APPLICANT:
                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                            4404 CATCGACAACTTCAACCAGCAGAAGAAAAGTTTGGAGGTCAGGACATCTTCAT 4457
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    Application US/09425043
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3401 HILLVIEW AVENUE, MS A2-250
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DIETRICH, PAUL S.
                DELGADO, STEPHEN
DIETRICH, PAUL S.
FISH, LINDA M.
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HERMAN, RONALD C.
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                                                      STEPHEN G.
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Pred. No. 2.2e-11;
0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 120;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 855-5322 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                 APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/425,043
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CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
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                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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ADDRESSEE:
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                   FISH, LINDA M.
HERMAN, RONALD C.
                                                                                                                                                           DIETRICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                           DELGADO, STEPHEN G. DIETRICH, PAUL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (650)
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Pred. No. 2.2e-11;
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STREET: 3401 HII CITY: PALO ALTO

3401 HILLVIEW AVENUE, MS A2-250

COUNTRY:

U.S.A.

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Sequence 2, AFF-
No. 6335172
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                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 6007 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: ROTELECOMMUNICATION INFORMATION: TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-FEB-19:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                               APPLICANT: HERMAN, RONALD C.
APPLICANT: SANCAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLIC
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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TOPOLOGY: linear
                                                                                                     STATE:
                                                                                                                       CITY: PALO ALTO
                                                                                                                                     STREET:
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                                                                                                                                       3401 HILLVIEW AVENUE, MS A2-250
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DIETRICH, PAUL S.
                                                                               U.S.A.
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                                                                                                                                                                                                                                                                                          FISH, LINDA M.
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                                                                                                                                                                                                                  I-SUBUNIT AND A SPLICE VARIANT THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 603081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.9%;
Best Local Similarity 69.0%;
Matches 120; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 852-3097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                              STREET: 3444
CUTY: PALO ALTO
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
PILING DATE: 26-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: R0020B-REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 94304-1397
                                                                                                                                                                                                                                                                      ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09024020B
                                                                                                                                                                                                                                                  3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                            HERMAN, RONALD C.
SANGAMESWARAN, LAKSHMI
VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                      FISH, LINDA M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                STEPHEN G.
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Pred. No. 2.2e-11;
0; Mismatches 53;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/039,447

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-024-020B-7
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Best Local Similarity
Matches | 120; Conserv
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 6556 base pair
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
PILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
PILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 6556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3401 HII
CITY: PALO ALTO
REGISTRATION NUMBER:
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94304-1397
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ilarity 69.0%;
Conservative
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISH, LINDA M.
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Pred. No. 2.3e-11;
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US-09-024-020B-43
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TELEFAX: (650) 855-5322 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                        APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                          CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SANGAMESWARAN, LAKSHMI
TITILE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
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Local Similarity 69.0%;
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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94304-1397
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EDNESS: single
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DIETRICH, PAUL S.
                                                          (650) 852-3097
                                                                                                                                                                                                                                                 16-FEB-1998
                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                   US/09/024,020B
                       43:
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Pred. No. 2.3e-11;
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US-09-024-020B-43
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Sequence 43, April
835172
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Best Local Similarity
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Query Match
                                                                                                                          INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 6586 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: ROTELECOMMUNICATION INFORMATION
TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                        FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SANGAMES TITLE OF INVENTION:
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FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 6
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: PALO ALTO
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                                                                                                           nucleic acid
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLI-
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                                                                           linear
                                                      DNA (genomic)
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                                                                                                                                                                               855-5322
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 18.9%;
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Pred. No. 2.3e-11;
 Score 77.2;
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Patent No. 603081
                                                                                                                     Best
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                                                                                                     Matches
                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 6826 base pairs
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 26-FEB-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 852-3097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                              NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                            TYPE:
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FILING DATE: 16-FEB-1998
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                                                                                                                       Local Similarity
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                                 4257 AGATTCCCGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACATGTACATCTA
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259 CTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT 318
                                                                     200 AAATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TT 258
                                                                                                                                                                                                                                       nucleic acid
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                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: US 60/039,447
26-FEB-1997
                                                                                                                                                                                       DNA (genomic)
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NOVEL CLONED TETRODOTOXIN-SENSITIVE
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                                                                                                                       Score 77.2; DB 3; Pred. No. 2.3e-11;
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RESULT 14 US-09-425-043-8

Patent No.

8, Application US/09425043 o. 6335172

GENERAL INFORMATION:
APPLICANT: DELGADO
APPLICANT: DIETRIC
APPLICANT: FISH, L

DIETRICH, FISH, LINDA M. HERMAN, RONALD C DELGADO, STEPHEN G.

PAUL S.

APPLICANT:

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CATTGACAACTTCAACCAACAGCAGAAAAAAGATAAGTATCTGGGTTGTCTTGAT 372

CATCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTTCAT 4430

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; MOLECULE TYPE: DNA (genomic)
US-09-425-043-8
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Best Local &
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APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 855-5322 INFORMATION FOR SEQ ID NO:
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ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6826 base pair
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ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
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TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
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                                                                                                                                                                  4257 AGATTCCCGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACATGTACATCTA 4316
                                                                                                           259 CTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT
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CATCGACAACTTCAACCAGCAGAAGAAAAGTTTGGAGGTCAGGACATCTTCAT 4430
                                       CATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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Pred. No. 2.3e-11;
0; Mismatches 53;
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APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG OT SYNDROME GENES KVLQT1 AND
TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
                                                                                                                                                                                                                                                   Query Match 18.7%;
Best Local Similarity 71.0%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No: 6342357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2323-155
CURRENT APPLICATION NUMBER: US/09/634,920
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/190,057
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/147,488
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
4419 CAACCAACAGAAGAAAAGTTAGGGGGCCAGGACATCTTCAT 4460
                                                                                  4359 CATCATCTTTGGGTCTTTCTTCACCCTGAACCTCTTTATTGGTGTCATCATTGACAACTT 4418
                                                                                                                                                                     4299 GTATGAAGAGCAGCCTCAGTGGGAATACAACCTCTACATGTACATCTATTTTGTCATTTT
                                     331 CAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                  212 GAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCTTCGTAGTCTT
                                                                                                                 271 TATCATCTTTGGCTCATTCTTCACTCTGAATCTTCTTCATTGGCGTTATCATTGACAACTT
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                                                                                                                                                                                                                                                     Score 76.4; DB 4;
Pred. No. 3.6e-11;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                  DB 4; Length 6048;
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Search completed: March 22, 2004, 23:17:52 Job time : 57.7479 secs

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Minimum DB
Maximum DB
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No.
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112.8
81.6
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
               seq length: 0
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                                                                                                Issued_Patents_NA:*

| Compared_Patents_NA:*
| Compare
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US-09-354-147C-6

US-09-354-147C-4

US-09-354-147C-1

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US-08-843-417-9

US-09-527-013-9
                                                         US-09-024-020B-8
US-09-024-020B-9
US-09-024-020B-1
US-09-024-020B-1
US-09-024-020B-2
US-09-024-020B-2
US-09-024-020B-2
US-09-024-020B-2
US-09-024-020B-3
US-09-024-020B-43
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Million cell updates/sec
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Sequence 41, Appli
Sequence 4, Appli
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Sequence 43, Appli
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## ALIGNMENTS

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; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human NaN
US-09-354-147C-41
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US-09-354-147C-41
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SEQ ID NO 41
                                                                                                                                                                                                                                                                                                      Best Local Sin
Matches 192;
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
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4336
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                                                                                                              190
                                                                                                                                                                        130 CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                                                                                                                                                                                                                      Similarity
                                                                                                        GTCGTGCTTCTTTCCATTGTTAGTA 4360
                      GTCGTGCTTCTTTCCATTGTTAGTA 274
                                                                        Conservative
                                                                                                                                                                                                                                                                                                    Score 163.4; DB 4
Pred. No. 3.2e-39;
0; Mismatches 11
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                                                                            4335
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-09-354-147C-6

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GENERAL INFORMATION:

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Maxman, Stephen G.

ITILE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/09/354,147C

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR APPLICATION NUMBER: D67/109,402

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver: 2.1
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                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 4
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Matches 160; Conserv
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                                                                                                                                                                                                                                 APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
                                                                                                                 PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: y = c
OTHER INFORMATION: Leu.
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LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
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ORGANISM: Homo sapiens
TYPE: DNA
ORGANISM: Mus musculus
                                        ENGTH: 5822
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Pred. No. 1.2e-29;
0; Mismatches 11
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APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
FITLE OF INVENTION: Modulation of Sodium Channels in Dor
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION UMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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; LCCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse NaN, n = a or c or g or
US-09-354-147C-4
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Best Local
                                                                                                                                              Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (41)...(5335)
OTHER INFORMATION: cDNA sequence for
                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1996)..(4042)
OTHER INFORMATION: n = a or c or g
OTHER INFORMATION: 652 is Leu; Xaa
OTHER INFORMATION: or Lys.
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5875
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCATION: (19) .. (5313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4153
                                                                4111 CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA 4168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4095 AAACATGATTATCATGATGGCTGAATCTGAAGGCCAGCCC--AACGAAGTGAAGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
                                                                                                                                                                Similarity
TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCAAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCTTTCCATCATTAGTA 4291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGATATTCTCAACATAGTCTTCGTGGTCATCTTTACCGTAGAGTGTCTCATCAAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTCGTG
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                                                                                                    CTANACCATGATTGGCTTGATGGCCTANATATACANCCANCCCCANAGCCATGGAATCCA 132
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75.7%;
                                                                                                                                           Score 112.8; DB 4;
Pred. No. 5.8e-24;
0; Mismatches 47;
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Pred. No. 5e-24;
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US-08-843-417-9
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Best Local Similarity
Matches | 102; Conserv
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                                                                                                                                                                                                                                                                                                                TOPOLOGY: unk
MOLECULE TYPE:
HYPOTHETICAL: N
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MEDIUM TYPE FIDDBY disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 5874 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415)-324-7041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: unknown
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                                                                   583
                                                                                                                                       523
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                                                                                         TIGCTITGAGGCAATACTACTICACCAATGGCTGGAATTTATTTGACTGTGTGGTCGTGC 256
                                                                                                                                       TGGGCAAAATCAACCAGTTCTTTGTGGCCGTCTTCACAGGCGAATGTGTCATGAAGATGT
                                                                                                                                                             TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCT 196
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                                                                   TCGCTTTGAGGCAGTACTTCACAAATGGCTGGAATGTGTTTGACTTCATTGTGGTGG 4642
TTCTCTCCATTGCGAG 4658
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Fish, Linda M
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MENTION: CLONED PERIPHERAL NERVE
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                                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                         Score 81.6; DB 3;
Pred. No. 1.5e-14;
0; Mismatches 34;
                                                                                                                                                                                                                                            Length 5874;
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Patent No. 6479259
GENERAL INFORMATION:
                                                                                                                                                                                                                                             Matches 102;
                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/843,417
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
operating SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,013
FILING DATE: 16-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                               4583 TCGCTTTGAGGCAGTACTACTTCACAAATGGCTGGAATGTGTTTGACTTCATTGTGGTGG 4642
                                                                                                                                                              4523 TGGGCAAAATCAACCAGTTCTTTGTGGCCGTCTTCACAGGCGAATGTGTCATGAAGATGT
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ADDRESSEE: Heller Ehrman White & McAuliffe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                     197
                                                                                                                                                                                                  137 TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCT
                                                                                                                                                                                                                                                                Similarity
                             TTCTTTCCATTGTTAG
                                                                                                               TIGCTITGAGGCAATACTACTICACCAATGGCTGGAATTTATTTGACTGTGTGGTCGTGC 256
TTCTCTCCATTGCGAG 4658
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5874 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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OF INVENTION: CLONED PERIPHERAL NERVE
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                          13.9%; Score 81.6; DB 4; 75.0%; Pred. No. 1.5e-14; tive 0; Mismatches 34;
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RESULT 7 US-09-024-020B-8

Sequence 8, Application US/09024020B

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                                                                                                                    Sequence 8, Appr. No. 6335172
                                                                                                          Patent No. 6335172
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                      APPLICANT:
APPLICANT:
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LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILLING DATE: 16-FEB-1998
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0
TELECOMMUNICATION INFORMATION:
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   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                         208 CAATACTACTTCACCAATGGCTGGAATTTATTTGACTGTGGTGGTGCTTCTTTCCATT 267
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                                                                                                                                                 Application US/09425043
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                                                                                                                                                                                                                                                                                 GTTAGTAAGT 277
                                                                                                                                                                                                                                                                                                                      CACTACTACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATCCTCCATT
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                                                  DELGADO, STEPHEN G.
DIETRICH, PAUL S.
FISH, LINDA M.
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SANGAMESWARAN, LAKSHMI
/ENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                      RONALD
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75.4%;
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Pred. No. 1.1e-13;
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RESULT 9
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                                                                                                                                                                                                                                                     Sequence 5, Applic Patent No. 6030810 GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650) 855-532
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICANT: DELGAL...
APPLICANT: DIETRICH, PAUL J.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
APPLICANT: SANGAMESWARAN, LAKSHMI
APPLICANT: SANGAMESWARAN, TAKSHMI
APPLICANT: SANGAMESWARAN, TAKSHMI
APPLICANT: SANGAMESWARAN, TAKSHMI
APPLICANT: SANGAMESWARAN, TAKSHMI
APPLICANT: SANGAMESWARAN, THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/024
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION.

PRIOR APPLICATION NUMBER: US 09/024,020

**DFITCATION NUMBER: 1998

- 16-FEB-1998
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 111
MOLECULE TYPE:
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ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6826 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4660 AATCTGGTCTTTGTCATCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGA 4719
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94304-1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 60/039,447
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Pred. No. 1.1e-13;
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Best Local &
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEPAX: (650) 852-3097
TELEPAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
companyments. ciple
              ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                    APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRENT APPLICATION NUMBER: US/09/02*, ***-
PILING DATE: 16-FEB-1998
CLASSIFICATION: 536
CRIOR APPLICATION DATA:
RIOR APPLICATION DATA:
RIOR APPLICATION NUMBER: US 60/039,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                           5, Application US/09425043
o. 6335172
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97; Conserv
                                                                                                                                   PALO ALTO
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                                                                                                   U.S.A
                                                                                                                                                                                                                                                                                        FISH, LINDA M.
                                                                                                                                                                                                                                                                                                       DELGADO, STEPHEN G. DIETRICH, PAUL S.
                                                                                                                                                                                                                                                                         HERMAN
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                      RONALD C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.2%;
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Pred. No. 1.
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Version #1.30
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1.2e-13;
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US-09-024-020B-1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 855-5322 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                               ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                               APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
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                                  CLASSIFICATION:
                                                                                                                                                                                                                           CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                           COUNTRY:
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97; Conserv
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                                                                                                                                                                                                                                                                                                                               SANGAMESWARAN, LAKSHMI
VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THERBOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                 LINDA M.
                                                                                                                                                                                                                                                                                                                                                                                    RONALD C
                                                                                                                                                                                                                                                                                                                                                                                                                     H, PAUL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 77.2; 74.6%; Pred. No. 1
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US 60/039,447
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ATTORNEY/AGENT INFORMATION:

JANET P.

FILING DATE: 26-FEB-1997

NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:

34,799

R0020B-REG

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RESULT 12
US-09-425-043-1
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Matches 97; Conserv
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
APPLICATION NUMBER: US 60/039,447
FILING DATE: 16-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
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LENGTH: 5977 base pairs
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ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
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APPLICANT: FISH, LIN
APPLICANT: HERMAN, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLIC
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 94304-1397
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STRANDEDNESS: single
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                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4687 AATCTGGTCTTTGTCATCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGA 4746
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HERMAN, RONALD C.
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                        R0020B-REG
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Pred. No. 3.2e-13;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
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Best Local &
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                                                               TELEFAX: (650) 855-53
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                             REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: RO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                   APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
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                                              SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
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1 Similarity 74.6%;
97; Conservative
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94304-1397
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VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
VENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
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FISH, LINDA M.
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                                                                                                  (650) 852-3097
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                                                                               855-5322
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Pred. No. 3.2e-13;
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                                                                                                                                                                                         APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: 70/20B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEPHONE: (650) 852-3097
INFORMATION FOR SEQ ID NO: 2:
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 6007 base pairs
TYPB: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
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TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                        MOLECULE TYPE: DNA (genomic)
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les 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/425,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1397
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Similarity
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                  13.2%;
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Score 77.2; DB 4;
Pred. No. 3.2e-13;
0; Mismatches 33;
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Pred. No. 3.2e-13;
0; Mismatches 33;
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US-09-024-020B-7
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                                                                                                                                               Matches
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Best Local
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APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ANDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 16-FEB-1998 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                       LENGTH: 6556 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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                                                                     4834 AATCTGGTCTTTGTCATCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCCTTGAGA 4893
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                                                                                           148 AACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCAAAATCTTTGCTTTTGAGG
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                                208 CAATACTACTTCACCAATGGCTGGAATTTATTTGACTGTGGTGGTGGTGCTTCTTTCCATT 267
                                                                                                                                               97;
                                                                                                                                                              Similarity
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DIETRICH,
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SANGAMESWARAN, LAKSHMI
VENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                            13.2%; Score 77.2; DB 3; 74.6%; Pred. No. 3.3e-13;
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                                                                                                                                               Mismatches
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Search completed: March 22, 2004, Job time : 80.7372 secs	GTTAGTAAGT         GTGGGAATGT
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Title:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfIles1.seq:*
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           DB
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      US-09-354-147C-41
US-09-354-147C-1
US-09-354-147C-1
US-09-354-147C-3
US-09-224-426-3
US-09-478-601-3
US-09-478-602-3
US-09-489-039A-4251
US-09-489-039A-4251
US-09-616-750A-72
US-09-616-289-16
US-08-061-376-2
US-09-616-289-16
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US-09-616-289-16
US-09-616-289-16
US-09-313-294A-3811
US-09-313-31-721-58
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Sequence 41, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 2256, Ap
Sequence 725, Ap
Sequence 725, Ap
Sequence 791, Ap
Sequence 7991, Ap
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 15, Appli
Sequence 25, Appli
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Sequence 25, Appli
Sequence 25, Appli
Sequence 258, Appli
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J , 0	, , ,	Query Best I Matche	PRIOR FILIN PRIOR APPLI PRIOR FILIN PRIOR FILIN PRIOR FILIN NUMBER OF S SOFTWARE: P SEQ ID NO 41 LENGTH: 58 TYPE: DNA ORGANISM: FEATURE: PRATURE: NAME/KEY: LCCATION: OTHER INFO OTHER INFO OTHER INFO	SSULT 1  9-354- 9-354- Patent N GENERAL APPLICA APPLICA APPLICA TITLE O TITLE RE CURRENT CURRENT CURRENT PRIOR A	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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TCCACGC	GGAGACT	90.0 Similarity 97.7 4; Conservative CAAGGTGGACCAAAAT	TILING DATE: 1998 APPLICATION NUMBE TILING DATE: 1998 APPLICATION NUMBE TILING DATE: 1999 OF SEQ ID NOS: 4 RE: PATENTIN VET. 40 41 1: 586 DNA SM: Homo sapiens ES: ES: CEY: CDS CON: (31)(5403) INFORMATION: full 1.47C-41	RESULT 1  US-09-354-147C-41  US-09-354-147C-41  Sequence 41, Application US/09354147( Patent NO. 6573067  GENERAL INFORMATION: APPLICANT: Dib-Hajj, Sulayman; APPLICANT: Waxman, Stephen G. TITLE OF INVENTION: Modulation of SC FILE REFERENCE: 44574-5004-01-US; CURRENT APPLICATION NUMBER: US/09/31; CURRENT FILING DATE: 1999-07-16; PRIOR APPLICATION NUMBER: US 66/072,	11111111111111111111111111111111111111
CTACCTC	TGTCTAG	90.0 97.7 vative CCAAAAT          CCAAAAT	IUMBER: U 1998-11- 1998-11- IL99-01- NS: 4-4 Ver. 2.1 Ver. 2.1	ion US/ Sulaym Sulaym Stephen Modulat 4-5004- 4-509- 1999-	1812 4079 41132 4204 4204 474 3701 4503 4503 4503 4503 4503 4503 4503 4503
ATAGCT	CTTTGG	%; Sco %; Pro o; GACTTG	1-29 1-20 PCT/US99/02 1-29	AL 093541477 093541477 an G. G. 10n of S. 01-US US/09/3 07-16 07-16 S. 60/072	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
CACAGO	GETGGCC	Score 200.6; Pred. No. 7. Pred. No. 7. ); Mismatche TTGGGAAAACGGG	. 2 4	ALIGNMENTS 47C 50dium Ch 80dium Ch	09-023-09-023-09-030-09-030-09-030-09-030-09-033-09-033-1-09-175-09-175-09-175-09-08-080-09-09-09-09-09-09-09-09-09-09-09-09-09
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TCAGCCTC	AGGTCCAC	4; Ler 3; Inc 4; Inc ATTCACCA	for human	ls in Do	35 36 3
TGAGCTC	ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCA	90.0%; Score 200.6; DB 4; Length 5860; imilarity 97.7%; Pred. No. 7.4e-58; Conservative 0; Mismatches 4; Indels 1; Gaps CAAGGTGGACCAAAATGACTTGGGAAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA	NaN	Dorsal Root	Sequence Sequence
CAGGGG	GAGCCC         GAGCCC CAGGGG	0; Gap			nce 12 nce 13 nce 12 nce 13 nce 13 nce 23 nce 25 nce 25 nce 27 nce 27 nce 44 nce 44 nce 44
TCA 5473		5 6 4 5 3		Ganglia	430, App 1008, Ap 11092, Ap 3486, Ap 34
73	2 4 4 4	1;			

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GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
ITILE OF INVENTION: Modulation of Sodium Channels in
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: DE 60/109,402
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: DCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOSTWARE: Patentin Ver. 2.1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
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Best Local Similarity
                                                                                     CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF CENTROLOGY
                                                                                                                                                                                                                                                 FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
                                                    SOFTWARE:
                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1996). (4042)
OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.
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LOCATION: (41).
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                                                       PatentIn Ver.
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74.3%;
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Pred. No. 4.5e-24;
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US-09-478-601-3/c; Sequence 3, Application; Patent No. 6221616

US/09478601

GENERAL INFORMATION:

APPLICANT: Salon, John APPLICANT: Laz, Thomas

APPLICANT: Nagorny, Raisa

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LCCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse
US-09-354-147C-4
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Best Local Similarity
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APPLICANT: Laz, Thomas M
APPLICANT: Nagorny, Raisa
APPLICANT: Wilson, Amy E
APPLICANT: Wilson, Amy E
APPLICANT: Wilson, Amy E
APPLICANT: Wilson, DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 57453/JPW/JHB
CURRENT APPLICATION NUMBER: US/09/224,426
CURRENT FILING DATE: 1998-12-31
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                      LENGTH: 1214
TYPE: DNA
ORGANISM: rat
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                                                                                                                                    1138 ATCTCTCCCCACGGTTTGATGGGGTGGCCTGACTTGGAGGCGACTGGGGAATTGTCAGGT 1079
                                                                                                 105 CCACTGTGACTGAGCCTTCACCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCCTTCAG 164
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                               CCTCTGAGCTCCAGGGGTCA 184
                                                                 GCCTTTGCTTTCTGTCCTCTCCTCATCAGCTGTCTGAGCGTTGCTGACCGTGCGGAGCTG
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CCCCTGGGCTGCAGGCTTCA 999
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52.1%;
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71.1%;
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Pred. No. 2.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                        ; ORGANISM: Rattus norvegicus US-09-478-602-3
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APPLICANT: Salon, John A.
APPLICANT: Laz, Thomas M.
APPLICANT: Hagorny, Raisa
APPLICANT: Wilson, Amy E.
APPLICANT: Wilson, Amy E.
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 57453y\JPW
CURRENT | APPLICATION NUMBER: US/09/478,602
CURRENT | FILING DATE: 2000-01-06
EARLIER | APPLICATION NUMBER: 09/224,426
EARLIER | FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 15
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Matches
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SEQ ID NO 3
LENGTH: 1214
TYPE: DNA
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LENGTH: 1214
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Best Local
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Best Local Similarity
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ORGANISM: Rattus norvegicus
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CCCCTGGGCTGCAGGCTTCA 999
                                  CCTCTGAGCTCCAGGGGTCA 184
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ilarity 52.1%;
Conservative
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US-09-489-039A-4251
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US-09-489-039A-4251/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILL REPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2256
LENGTH: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PAREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 4251
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Patent No. 6610836
                                                                                                                                                                                                                                           Query Match
Best Local :
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                              ENGTH: 1152
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                                                                                                                                                                                                                                             Local Similarity
                                   212
                                                                                                                                                    286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
166
                                                                                                            152 GCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCTTAGTGTATCAACAGGGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 ACCCCGAAAGCCTGCCCTCAGCGGCAGCGGTCAGCAGGTGGATGGCGTTATAAATATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 GCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCTTAGTGTATCAACAGGGAGTGG
                                                                                                                                                                                      92 CCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTCATAGCTTCACA 151
                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 CCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTCATAGCTTCACA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conserv
                                                                         ACCCCGAAAGCCTGCCCTCAGCGGCAGCGGTCAGCAGGTGGATGGCGTTATAAATATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCACC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGGGCGAACGCTCCCCGGACCACATCATATTCTCCAGACCGCCCTCTTCGCTGATAA
                                     ATTCACC 218
                                                                                                                                                  CGAGGGGGGAACGCTCCCCGGACCACATCATATTCTCCAGACCGCCCTCTTCGCTGATAA
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%;
ilarity 52.8%;
Conservative
                                                                                                                                                                                                                                                                                                                      pneumoniae
                                                                                                                                                                                                                                           13.9%;
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                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                           Score 31; DB 4
Pred. No. 0.77;
0; Mismatches
                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1152;
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US-09-154-750A-72/c

Sequence 72, Application US/09154750A Patent No. 6432640

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9791
LENGTH: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9791, Applic Patent No. 6639063 GENERAL INFORMATION:
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 72
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
-09-621-976-9791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: p53-Induced Apoptosis
FILE REFERENCE: 1107.75357
CURRENT APPLICATION NUMBER: US/09/154,750A
CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/079817 PRIOR FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 842
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338
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                                    141 ATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAGCCCTCACCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTG 170
256 AGCCCATTCCGGCCCCCATCTCACCCAAGATCCCCAGAGTCCAGGAGCT 305
                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 CTCTTTGCAATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                   l Similarity
60; Conserv
                                                                          CTTTGAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCCAGCCTCACCCCTGCCCC
                                                                                                              CTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCCCACCCAGCCTCTGCCTTCCATCCACATCTTCTCACGCAGCCTCTG
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                                                                                                                                                   Conservative
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53.9%;
                                                                                                                                                                     13.5%;
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                                                                                                                                                 Score 30; DB 4; Length 425; Pred. No. 1.1; o; Mismatches 50; Indels
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Pred. No. 1.
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RESULT 11

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                                                                                                                                          Sequence 16, Application US/08979608A Patent No. 6355451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08061376 Patent No. 6175000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1147 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 13-MAY-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Reiter, StepherestraTION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
               Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES:
                                                                                                                       APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                     1017 CAACAAAAGCTGTCAGAACTTGCTTCAGAGAAATCTGCAGCTCTTTTTCAAGGGCCAGTC 958
                                                                                                                                                                                                                                                                                                         135 TACCTCATAGCTTCACAGCCTTGCCTTCAG 164
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                                                                                                                                                                                                                                                                                                                                                                                 GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAATGACTTGGGAAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                                                                                                                                                                                                                                                                               GCCACTCTGCAGGGTGCCGCTCAGTACAGTTCACACAAGTGTAGGCCACACTTTCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1147 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pretty, Schroeder, Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Djabali, Malek
Selleri, Licia
Parry, Pauline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evans, Glen A.
                                                                                     Law, Simon W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFO... 31,192
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                                                                                                          Robert S.
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 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 3; Length 1147; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
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                                    IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 13
US-09-517-849-16
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                                                                                                                                                                                                                                                                                                                      Sequence 16, Application Patent No. 6605588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
TREATING ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MYETB, LOUIB
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                  NUMBER OF SEQUENCES: 42
CORRESONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                      APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 CTTTGGGGTGGCCAAGGCCAAGGTCCACTGTGACCTGAGCCCTCACCTCCACGCCTACCTC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTTGAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCCCCAGCCTCACCCCTGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCCATTCCGGCCCCCATCTCACCCAAGATCCCCCAGAGTCCAGGAGCT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatik
OPERATING SYSTEM: DOS
                                                                 STATE: MA
                                                                                 CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                   Application US/09517849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                              Lees, Robert
Law, Simon W.
                                                                                                                                                                                                                                               Arjona, Anibal A.
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                                                                                                                                                                                                                                                                                   Robert S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10797-002001 (formerly 3983/59818)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-517-849-16
                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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                                                                                              SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16,
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Best Local Similarity 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
                                                                                                             NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Ann M.
                                                                                                                                                                  PRIOR FILING DATE: 1997-06-03
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-870
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Myers, Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
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                                                                      1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/979,608 FILING DATE: 26-NOV-1997
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09616289
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US-09-616-289-16
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Best Local Similarity
Matches 60; Conserv
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Patent No. 6175000
                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                Best Local Similarity Matches 75; Conserv
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APPLICANT: Evans, Glen A.
APPLICANT: Djabali, Malek
APPLICANT: Selleri, Licia
APPLICANT: Selleri, Licia
APPLICANT: Parry, Pauline
TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11023
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/061
FILING DATE: 13-MAY-1993.
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619)546-9392
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DADITOTON NIMBER: 18/08/061 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 444 South
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2429 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 90071
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                                                                                                                                       1017 CAACAAAAGCTGTCAGAACTTGCTTCAGAGAAATCTGCAGCTCTTTTTCAAGGGCCAGTC 958
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135 TACCTCATAGCTTCACAGCCTTGCCTTCAG 164
                                             957 GCCACTCTGCAGGGTGCCGCTCAGTACAGTTCACACAAGTGTAGGCCACACTTTCTGGCA 898
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                                                                                                                                                                           15 CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                      GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Pretty, Schroeder, Brueggemann & Clark 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                              13.5%; Score 30; DB 3; Length 2429; llarity 50.0%; Pred. No. 2.3; Conservative 0; Mismatches 75; Indels
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Db 897 GATTAGATAGAATCTCATACTCTCTG 868

Search completed: March 22, 2004, 23:17:57 Job time: 34.3955 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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1: gb ba:*
2: gb ht:*
3: gb ht:*
5: gb ov:*
6: gb pat:*
9: gb pi:*
9: gb pi:*
9: gb vi:*
11: gb sts:*
12: gb sts:*
12: gb sts:*
12: gb sts:*
13: gb un:*
14: gb vi:*
15: em ba:*
6: em fun:*
9: em ow:*
16: em ow:*
17: em ow:*
18: em ow:*
19: em ow:*
10: em ow:*
11: em ow:*
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12: em ba:*
13: gb un:*
14: em ht:*
15: em ba:*
16: em ht:*
17: em ow:*
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is the number of results predicted by chance to have a
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 c 3	0.821 Q	2800 I CH	0711-6	. 0 0 0 0   B	ID AX017227 BD138449 AC116038 AR340648	rip 722 844 603
		(48888888888	4. 4		HSA417790 BD0012083 BD0082952 AF150882 AR340678 AF188679 BD0012082 BD0012082 BD0012082 BD0012082 AF109737 AC124662	90
c 16	<sup>1</sup> . <sup>2</sup> . <sup>2</sup> .5.5.		11 10 10 10 10 10 10 10 10 10 10 10 10 1	500001	AC127824 AC127815 AC127215 AR340647 BD217792	AC127824 Rattus no AC127215 Rattus no AC127215 Rattus no AR340647 Sequence BD217792 Regulation are allocated at the action of th
22222	44.55.00 45.00 45.00 45.00 45.00 45.00	222222	5849 5875 5875	, o o b o b	AB031389 E36125 RNO237852 AR340646 BD217791 AX017217	AB031309 mus mus E36125 Nucleic ac AJ237852 Rattus AJ237856 Sequence BD217791 Regulati AX017217 Sequence
27 29 30 31 32 33	45.8 45.8 37.6 37.6	21.3 21.3 21.3 17.5 17.5 16.9	5897 5905 5908 182506 194050 171363 172879	0 N N 0 0 H 0	BD138440 AF059030 B36122 AL359077 AL359077 AL354658 BX470146 BX9000213	9030 9030 2 Nu 077 658 146
	1	16.5 16.2 16.2	7021 7021 8409 8601 7676 2197	0 00 00 00 00	82 82 83 83 83 83 83 83	114 113 110 110
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		16.2 16.2 16.1 16.1 16.0	244/221 248639 253625 169207 233925 202214 243500	222522	AC135768 AC135768 AC098417 AC119813 AC118930 AC135818 AC100177	68 17 813 30 18
45	34.4	16.0	4350	N	$\sim$	1001

## ALIGNMENTS

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TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX017227	KESOLI L
Mammalian sodium channel proteins Patent: WO 9947670-A 11 23-SEP-1999;	Tate, S.N., Grose, D.T. and Hick, C.A.	-	Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX017227.1 GI:10042147	AX017227 .	Sequence 11 from Patent WO9947670.	AX017227 215 bp DNA linear PAT 07-SEP-2000		

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Best Local Similarity
Matches 215; Conserv
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PN JP 2002508941-A/10
PD 26-MAR-2002
PD 26-MAR-2099
PF 18-MAR-1999 JP 2000536853
PF 18-MAR-1998 GB 9805793.8
PI DAVID THOMAS GROSE, CARCLINE ANNE HICK, SIMON NICHOLAS TATE
C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: JP 20025
GLAXO GROUP LTD
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Grose, D.T., Hick, C.A. and Tate, S.N.
Mammalian sodium channel protein
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                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Box 352145, Seattle, WA 4 (bases 1 to 167476) Kaul,R.K., Olson,M.V., 2 Saenphimmachak,C., Buckl
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AC116038.3 GI:37537604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-OCT-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Oct 7, 2003 this sequence version replaced gi:21622736.
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Direct Submission
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Kaul,R.K., Olson,M.V., Raymond,C.
Direct Submission
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Kaul, R.K., Olson, M.V., Zhou, Y.,
Saenphimmachak, C., Euckley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-JUN-2002)
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                                                   Center project name: chr-3
Center clone name: RP11-134J21 (bc0780)
Center clone name: RP11-134J21 (bc0780)
Center clone name: RP11-134J21 (bc0780)

Sequencing vector: plasmid; 100% of reads chemistry: Dye-terminator ET; 45% of reads chemistry: Dye-terminator Big Dye; 55% of reads consensus quality: 167467 bases at least Q40 consensus quality: 167476 bases at least Q20 consensus quality: 167476 consensus
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                               Insert size: 167476; sum-of-contigs
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Buckley,D., Kibukawa,M.,
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WA 98195, USA
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WA 98195, USA
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Kibukawa,M.,
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Buckley,D.,
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Kibukawa, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rouse, G., Wu, Z., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 07-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raymond, C.
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75 4167 999 990 2 72 <800 3014 3028 8 40 6560 4721 4667 2 10 4771 727 745 4 68 3447 179 <800 2 87 <800 7123 7158 2 87 <800 7123 7158 2 88 391 2078 2040 5 68 391 1891 1888 6 62 <800 1891 1888 6 63 <800 8072 8171 4	fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.  Begnermap FngrPrnt SeqDermap FngrPrnt SeqDermap FngrPrnt  SeqDermap FngrPrnt SeqDermap FngrPrnt SeqDermap FngrPrnt  6 <800 6382 6514 2067 2008  2248 2299 512 <800 2317 2259  2248 2299 512 <800 2317 2259  2016 2003 2707 2741 2813 2744  4889 4771 4809 4878 2537 2550  3455 3447 184 <800 1923 2008  225 <800 5818 5899 2486 2550  72 <800 1364 1346 4036 3992	Overlapping Sequences: 5': RP11-114A3 AC137625, 2001-bp overlap 3': RP11-182A24 (UWGC:bc0782) AC123903, 41341-bp overlap 41341-bp overlap 4141-bp overl
309 	2709 19834 19834 8729 8729 2264 651 7181 6166	5080 6613 8963 8963 331 2328 2328 2038 712 1368 1168 11620 775
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<800	2686	
7414 822	2686	5088 6560 9211
<ul> <li>&lt;800</li> <li>7414</li> <li>7557</li> <li>822</li> <li>511</li> <li>&lt;800</li> <li>602</li> <li>&lt;800</li> <li>766</li> <li>1501</li> <li>1555</li> <li>6843</li> <li>6824</li> <li>2033</li> <li>2040</li> <li>5401</li> <li>5397</li> <li>587</li> <li>&lt;800</li> </ul>	2686 5528 19753 475 8629 2310 2299 5177 <800 391 7213 166 6159 3594 <800 1172 8629 316 <800 1172 98629 316 <800 4023 3718 1975 3718 324 9792 1341 <800 4463 8629 3569 1560 1229	5088 92 6560 3674 9211 5478

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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VERSION
KEYWORDS
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AR340648
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ORGANISM
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BD217793
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OS Homo sapiens (human)

PN J 2002509860-A/3

PD 02-APR-2002

PF 29-JAN-1999 JP 2000529355

PR 29-JAN-1998 US 60/072990,20-NOV-1998

SULAYMAN DIB HAJJ,STEPHEN WAXMAN
                                                                                                  1 (bases 1 to 3701)
Hajj, S.D. and Waxman, S.
Regulation of sodium channel in posterior
Patent: JP 2002509860-A 3 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 3701)
Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in
Patent: US 6573067-A 6 03-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6
AR340648
                                                                                                                                                                                                                    BD217793.1 GI:33027563 JP 2002509860-A/3.
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Regulation of sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          Homo sapiens
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/mol_type="genomic DNA"
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97.7%;
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patent US 6573067
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Pred. No. 1.5e-16;
0; Mismatches 3;
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Pred. No. 1.9e-40;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSA417790 5419 bp mRNA linear Homo sapiens mRNA for voltage-gated sodium channel AJ417790 GI:22796539 NAV1.9 gene; voltage-gated sodium channel. Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-OCT-2001) Blum R.,
                                                                                                                                                                                                                                                                                                                  Blum, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                              Nature 419
22272672
                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                          Ludwig-Maximillians-Universitaet, 608, 80802 Muenchen, GERMANY
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C07K16/18,
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                                                                                    excitation"
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cell_type="room"
                                                                                                                                                                                                                                                         Location/Qualifiers
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/evidence=experimental
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                                                                    note="TTX-insensitive"
                                                                                                                                                                                                    db_xref="taxon:9606"
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96.8%;
                                                                                                                                                                         type="neuroblastoma"
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(922).
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Pred. No. 1.5e-16;
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db\_xref="GOA:Q8NDX3"

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BD012083
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...ammalla; Butheria; Primates; Craniata; Vertebrata; Euteleos
AUTHORS
TITLE
Human sodium channel SCN12A and Jeong,S.Y.
Human sodium channel SCN12A and SCN8A
JOURNAL
JAPAN SCIENCE AND TECHNOLOGY CORP,ICHIRO KANAZAWA,JUN GOTO, EON
YENT
OS Homo sapiens (human)
PN WO 0190355-A/2
PD 23-MOY-2000 WO 2000JP004f^^
PR 23-MAY-2000 JP n^^
PI ICHIRO K^**
                                                                                                                                                                                      COMMENT
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Human sodium channel SCN12A and
BD012083
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92; Conserv
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CLKIIALDPYHYFRRGMNIFOSIVALLSFADVNNCVLQKRSWEPLRSFRVLRVFKLAK
SWPTLMTLIKIIGNSVGALGSLTVLVIVIFIFISVVEMQLFGRSFNSQKSFKLCNFR
PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENNWECMQEANASSSLCVIVFILITVIG
KLVVLNLFIALLINSFSNBERNONLEGBARKTKVQLALDFFRASCFVCHTLEHFCHK
WCRKQNLPQQKEVAGGCAAQSKDIIFLUWEMKRGSFYQESLGIIITSVPKTLGVRHDWI
MLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKFTSQRVQSVEIDMFSED
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IYAAVUSTEKEQQPEPESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNENQQXKLGG
QDIEWTEEGKKKYNAMKKLGSKKPQKPIFPENJKCQGLVFDIVTSQIFDIIIISLIIL
NMISMMAESYNQPKAMKSILDHLNWVEVVIFTLECLIKIFALRQYFTNGWNLFDCVV
VLLSIVSTMISTLENQEHIPFPTLFRIVRLARIGRILEFLYMAARGIRTLECLFQLSTSAG
PSLFWIGLLLFLIMFIYALLGNMWFSKVNPESGIDDIEWKTFASSMLCLFQLSTSAG
MDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENENTA
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SVDKRKPPWVIWMNLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVHLENQPKIQE
LLNCTDIIFTHIFILEMVLKWVAPGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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NLTLAVVTMAYEEQNKKVAAFELMESGKOOPFGSDSDEDCOKKPOLLEQTTKALSQNLSLD
SYFTPKKRKLFGNKKXKSFFLMESGKOOPFGSDSDEDCOKKPOLLEQTTKALSQNLSLD
HFDEHGDPLQRQRALSAVSILTITMKEQEKSQEPCLPCGENLASKYLVMNCCPQWLCV
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
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VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEFIVT
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/translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT
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Pred. No. 1.5e-16;
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AF150882 5728 bp mRNA linear PRI:
Homo sapiens voltage-gated sodium channel alpha subunit,
splice variant SCN12A-s (SCN12A) mRNA, complete cds.
                                                                                                                                                                                                                 92;
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Human sodium channel SCN12A
Patent: JP 2001327294-A 2 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5728)
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BD082952.1 GI:22628562
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27-NOV-2001
23-MAY-2000 JP 2000152085
ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
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                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Pred. No. 1.5e-16;
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1 (bases 1 to 5728)
1 deong/S.Y., Gotto,J., Hashida,H., Suzuki,T., Ogata,K., Masuda,N.,
1 Hirai,M., Isahara,K., Uchiyama,Y. and Kanazawa,I.
1 Identification of a novel human voltage-gated sodium channel alpha
2 subunit gene, SCN12A
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AF150882.1 GI:6693704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Location/Qualifiers
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HFDEHGDPLQRQRALSANSILTITIMKEGEKSQEECLEFGENLANGILLEQTKRLSONLSLD
HFDEHGDPLQRQRALSANSILTITIMKEGEKSQEECLEFGENLANGIGHLVPTSIFFLAM
KKULRTVMTDEPTELATICIIINTVELAMEHHKMEASFEKMLNIGHLVPTSIFFLAM
CLKIIALDPYHYFRRGMNIFDSIVALLSFADVANCVLQKRSWPFLRSFRVLRVFKLAK
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ETVLNILFIALLLNSFSNEERNGNLEGGBARKTKVQLALDRFRRAFCFVRHTLEHFCHK
WCRKONLPQXEVAGGCAAQSKDIIFLVMEMKRGSETOEELGIITSVFKTLGVRHDWT
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SVDKRKPPWVLWMLRKTCYQIVKHSWEESFIIFVILLSGALIFEDVHLENDFKIOE
SVDKRKPDWVLTWMLRKTCYQIVKHSWEESFIIFVILLSGALIFEDVHLENDFKIOE
CVDKRKPDWVLTWMLRKTCYQIVKHSWEESFIIFVILLSGALIFEDVHLENDFKIOE
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GEVPQPRPQLDLKASRKLJKLJGIPERLIGKFLEDLDFYRNHKTFMVLNRKRTIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNUTD
IAECVFTGIYIFEALIKILARGFILDEFSFLRODWNWLDSIVIGIAIVSVIPGITIKL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                                                                                                                                     LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
RTLRALRPLRALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGMMDI
                                                                                                                                                                                                                                                                                                                 IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
QDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKCQGLVFDIVTSQIFDIIISLIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLKTTGLYSVFFFIVVIFLGSFYLI
NLTLAVVTWAYEEQNKNVAAEIEAKEKWFQEAQQLLKEEKEALVAMGIDRSSLTSLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="voltage-gated sodium channel alpha subunit, alternat esplice variant SCN12A-s" /protein id="AAF24980 1" /db_xref="GI:6693705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="SCN12A"
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|mol_type="mRNA"
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chromosome="3"
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96.8%;
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                                                                                                                      Mismatches
                                                                                                                                             90.2; DB 9;
No. 1.5e-16;
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                                                                                                                                                                       Length 5728;
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           3206
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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LOCUS
DEFINITION
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MEDLINE
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Homo sapiens voltage-gated sc (SCN1A) mRNA, complete cds.
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Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal root ganglia
Patent: US 6573067-A 41 03-JUN-2003;
Location/Qualifiers
1. .5860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR340678
Sequence 41 from
AR340678
                                                                                                                                      2 (bases 1 to 6237)
Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman Direct Submission
Submitsion (21-SEP-1999) Neurology, Yale University/VAMC, 127A, Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                              Dib-Hajj,S.D., Tyrrell,L., Waxman,S.G.
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                               FEBS Lett. 462 (1-2), 117-120 (1999)
                                                                                                                                                                                                                                                                                 ganglion neurons
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                              Two tetrodotoxin-resistant sodium channels in human dorsal root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
                /map="3p21-p24"
/tissue_type="dorsal root ganglia"
1. .6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="unknown"
'gene="SCN11A"
                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                            1. .6237
                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:6572949
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96.8%;
                                                                                                                                                                                                   Tyrrell, L., Cummins, T.R., Black, J.A. and Waxman, S.G.
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patent US 65
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Pred. No. 1.5e-16;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                              Cummins, T.R.,
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type XI
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alpha subunit
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VERSION
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                         BD012082 6528 bp
Human sodium channel SCN12A and
BD012082
BD012082.1 GI:22092271
WO 0190355-A/1.
                                                                                                                                                                                                                                                                                                                 TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 140
                                                                                                                                                                                                                                                                                                                                                                                      AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 3037
                                                                                                                                                                                                                                                                                 TTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA 3072
sapiens (human)
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EPHLTIQDFRKKSDVTS ILSECSTIDLODGFGHLPEMVPKKQPEGCFPCC
SVDKRKEPMVIWMNLRKTCYQI VKHSWFESFII FVILLSSGALIFEDVHLENQPKIQE
LLNCTDII FTHI FILEMVLKWVAFGFGKYFTSAWCCLDFII VIVSVTTILINLMELKSF
RTLRALRALSQFEGMKVVWNALIGAI PAILMVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVLHYTI ITMKSQCESGRISMINGKVNFDNYGNAYLALLCVAIFKGWNDI
IYAAVDSTEKEQQPEFESNSLGYIYFVVFII FGSFFTLNLFIGVII DNFNQQQKKLGG
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PTVSCLRHWHMGDFWHSTLVVFRIILCGEWIENMWECMQEANASSGLCVIVFILITVIK
KLVVLNLFIALLLNSFSMEERNGNLFGGEAKKTKVQLALDFAFRRAFCFVBHTLEHFCHK
WCRKQNLPQQKEVAGGCAAQSKDIIPLVMEMKRGSETQEELGILTSVPKTLGVRHDWT
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HFDEHGDPLQRQRALSAVSILTITMKEGEKSQEFCLPGGENLASKYLVWNCCPQWLCV
KKVLRTVMTDPFTELATICIIINTVELAMEHHKMEASFEKMLMIGNLVPTSIFTAEN
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
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/rpt_family="Alu-Sc"
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NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
VLLSIVSTMISTLENQEHIPFPPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
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TEESEDPLGEDDFDIFYEVWEKFDPEATQFIKYSALSDFADALPEPLRVAKPNKYQFL
VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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Gevpqprpqldlkasrklpklygdifreligkpledldpfyrnhktfmvlnrkriiyr
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
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/gene="SCN11A"
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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/codon_start=1
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96.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 90.2; DB 9;
Pred. No. 1.5e-16;
0; Mismatches 3
                                                                                                             DNA
SCN8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 6237;
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                                                                                                                                             PAT 02-AUG-2002
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BD082951
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Query Match
Best Local Similarity
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1 (Dases 1 to 6528)

Kanazawa, I., Goto, J. and Tei, Y.
Human sodium channel SCN12A
Patent: JP 2001327294-A 1 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                              6528
Human sodium channel SCN12A.
BD082951
                                                                                                                                  Homo sapiens
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JP 2001327294-A/1.
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1 (bases 1 to 6528)
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                                                                                                                                 CDS
                                                                                                                                                                      23-MAY-2000 JP 2000152085
ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
                                                                                                                                                                                                                      Homo sapiens (human)
JP 2001327294-A/1
27-NOV-2001
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23-MAY-2000 JP 00P 152085
ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
C12N15/12, C07K14/47, C07K16/18
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/db_xref="taxon:9606"
                                                                                                              Location/Qualifiers (200) (5575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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42.0%;
96.8%;
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Score 90.2; DB 6;
Pred. No. 1.5e-16;
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Pred. No. 1.5e-16;
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Homo mapiens voltage-gated medium channel alpha medium than subunit SCN12A (SCN12A) medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jeong,S.Y., Goto,J., Hashida,H., Suzuki,T., Ogata,K., Masuda,N., Hirai,M., Isahara,K., Uchiyama,Y. and Kanazawa,I. Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6528)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-NOV-1998) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
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Location/Qualifiers
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                 NLTLAVVTMAYEEQNKNVAAEIEAKEKNFQEÄQGLLKEEKEALVAMGIDRSSLTSLET
SYFTEKKRKLFONKKRKSFTLÆSGKDØPEGSDSDEDCQKKFOLLEQTTKRLSQNLSLD
HFDEHGDPLQRQRALSAVSILTITMKEQEKSGEDEPCLPCESILÄSKYLVMNCCPØMLCV
KKVLRTVMTDEPTELÄITICIIITMKEQEKSGEDEPCLPCESILÄSKYLVMNCCPØMLCV
KKVLRTVMTDEPTELÄITICIIITVFLAMEHHKMEASSEKMLNIGNLVFTSIFIAE
CLKIIALDPYHYFRRGMNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
SWPTLNTLIKIIONSVGALGNLTVVLVIVIFIESESPAGKSEKLOPTG
PTVSCLRHWHMGDFWHSFLVVFRLICGEMIENWECNQEANASSSLCVIVFILITVIG
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MCRKQNLPQQKEVAGGCAAQSKDIIPLOMEMKRGSTOBELGILTSVPKTLGVBHDGWT
                                                                                                                                                                                                                                                                        IABCVETGIYIFEALIKILARGFILDEFSFLRDEWNWLDSIVIGIAIVSYIFGITIKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCN12A"
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1. .6528
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LLNCTD11FTH1FILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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Query Match Best Local S Matches 92 3207 3147 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 3206 141 81 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 140 Similarity TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175 TTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA 3241 Conservative 42.0%; 96.8%; 0 Score 90.2; DB 9; Pred. No. 1.5e-16; Mismatches <u>س</u> Length Indels 0

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REFERENCE AUTHORS KEYWORDS SOURCE RESULT 15 AC124662 LOCUS REFERENCE ACCESSION DEFINITION VERSION TITLE AUTHORS ORGANISM JOURNAL JOURNAL TITLE RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Changol, R., Cooke, B., Brown, A., Canagelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., BeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gardon, S., Gord, S., Gord, S., Goyette, M., Graham, L., Garand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Milool, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Retta, R., Pieback, M., Riley, R., Riec, C., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riec, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Survers, M., Travis, N., Trigillo, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct, Shhmission 1 (bases 1 to 241289)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RP24-409K22 AC124662.5 GI:38490569
HTG; HTGS\_PHASE1; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.
Mus musculus (house mouse) AC124662
241289 bp DNA linear HTG 22-NOV-20
Mus musculus chromosome 9 clone RP24-409K22 map 9, \*\*\* SEQUENCING
IN PROGRESS \*\*\*, 11 unordered pieces. Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Mus musculus Unpublished Direct Submission (bases 1 to 241289) ; Metazoa; Eutheria; Chordata; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. HTG 22-NOV-2003

REFERENCE

3 (bases 1 to 241289) Birren, B., Nusbaum, C., Anderson, M., Arachchi,

usbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.

FEATURES

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------ Project Information
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ADE11169_3	AAK65581	ADB60326	ABX60158	ABA07858	AAL03669	AAL37170	ABK42170	ABS99011	AAX13216	ADC87621	ADC86940	ABL03100	ADC10001	AAH89941	ADB48438	AAH90106	AAH90054	AAH14881	ADA69948	ABL29845	ADB72446
Continuation (4 of	Aak65581 Human imm	Adb60326 Connectiv	Abx60158 cDNA enco	Aba07858 Human ova	Aal03669 Human rep	Aal37170 Human mus	Abk42170 Genomic s	Abs99011 Enterococ	Aax13216 Enterococ	Adc87621 Human GPC	Adc86940 Human GPC	Ab103100 Drosophil	Adc10001 Human NOV	Aah89941 Human bon	Adb48438 Novel hum	Aah90106 Human bon	Aah90054 Human bon	Aah14881 Human cDN	Ada69948 Rice gene	Abl29845 Drosophil	Adb72446 Human ZFH

## ALIGNMENTS

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RESULT 1
   Best Local Similarity Matches 215; Conserv
               Query Match
Best Local
                                                                                      AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a
                                                                                                                                                                                                                                                                                                                                                                                                                    Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
                                                 Sequence 215
                                                                                                                                                                                         Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                                                                                          Grose DT, Hick CA,
                                                                                                                                                                                                                                                                                                                                              23-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                      WO9947670-A1
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human sensory neurone specific 2a nucleotide sequence fragment #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ21489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ21489 standard; cDNA;
                                                                           medicament
                                                                                                                                                                Claim 6; Page 67; 73pp; English.
                                                                                                                                                                                                                  WPI; 1999-562112/47.
                                                                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                           18-MAR-1998;
                                                                                                                                                                                                                                                                                                                    18-MAR-1999;
                                                                           for the treatment of pain or hypersensitivity
                                                   BP; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                             98GB-00005793
                                                                                                                                                                                                                                                                                                                    99WO-GB000838
                                                   A; 44 C; 48 G; 62 T; 0 U; 0 Other;
100.0%; +4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry
                    100.0%;
                                                                                                                                                                                                                                            Tate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215
                                                                                                                                                                                                                                            SN
               Score 215; DB 2;
Pred. No. 5.6e-61;
                            Length 215;
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Conservative

Mismatches

Indels

0,

Gaps

0

180 180 120 120 60 60

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RESULT 2
AAX87602
UXAKAZEXEKKK X8XEXEXEK KEK XEK KEK KEK XEX SOOOOOOOOOOOOOOOOOOOOOOO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX87602 standard; cDNA; 3638 BP
                                                                                                                                                                                                                             products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                         New isolated nucleic acids encoding sodium channels, used to develop
                                                                                                                                                                                                                                                               P-PSDB; AAY06598
                                                                                                                                                                                                                                                                                             Dib-Hajj S, Waxman
                                                                                                                                                                                                                                                                                                                                      29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                          05-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NaN; sodium channel; ion transport; human; dorsal root ganglia; paraesthesia; hyperexcitability; therapy; SCN11a gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1999
                                                                                                                                                                                                                                                                                                                  (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                         1999-479168/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGACAATGAGAAACTCCGTACTACTATGGTGAAAGAAGGTCTTAGTAAAAGGCACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGACAATGAGAAACTCCGTACTACTATGGTGAAAAGAGGTCTTAGTAAAAGGCACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGATTTTTCGTACCAACGGTTACGCTTCGAAGG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAATTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                      98US-0072990P.
98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                      99WO-US002008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NaN partial cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
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This is the nucleotide sequence of a partial cDNA clone which codes for a CC portion (see AAY06596) of human NaN, a previously unidentified voltage CC gated sodium channel protein that is preferentially expressed in dorsal CC root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R CC sodium current. The NaN channel cDNA was obtained from human DRG tissue CC DNA by PCR amplification (see also AAX87620-22). Rat, mouse and human CC UNAN nucleic acids (see AAX97600-02) and polypeptides (see AAX06596-98) CC are provided. The invention also includes expression vectors and CC transformed host cells, methods for identifying tissues and cells that CC express NaN, methods for identifying agents that modulate NaN channel CC activity or NaN channel mRNA transcription or translation, and a method CC using such agents to treat acute or chronic pain, paraesthesia and CC hyperexcitability phenomena. The preferential expression of NaN in CC sensory DRG and trigeminal neurons provides a target for selectively CC modifying the behaviour of these nerve cells while not affecting other correctly in the brain and spinal cord. The gene is named SCN11a Claim 1; Fig 8A1-2; 91pp; English.

Sequence 3638 BP; 1027 A, 793 Ç 801 G 1016 T; 0 ₽, 1 Other;

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RESULT 3
AAF30104
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The present sequence is that of a partial cDNA for a novel human CCC tetrodotoxin resistant sodium channel, termed NaN (see ARB20125). The CC cDNA was isolated from a human dorsal root ganglia tissue cDNA library by CC PCR amplification (see also AAF30122-23). A full-length seqvence is given contained protein family and produces a TTX-R sodium current. Such channels cunderlie the generation and propagation of impulses in excitable cells cunderlie the generation and propagation of impulses in extitable cells cannot neurons and muscle fibres. Preferential expression of NaN on cells sensory neurons innervating the body (dorsal root ganglia) and the face cells trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or cronic pain pathologies. A claimed method of treating pain, paraesthesia cand/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN concerned disparent to trigeminal neurons. NaN nucleic acids are used in centerapy to correct disparders associated with decreased sodium curression or (antisense) to down-regulate NaN expression, in the channel expression or (antisense) to down-regulate NaN expression, in the combinant production of NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 8A; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-2000; 2000WO-US019342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200105831-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF30104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-103147/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA 2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waxman
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/partial
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96.8%;
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Pred. No. 2.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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4.7

SXS

polypeptides

Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030

DB 4;

Length 3701;

Gaps

2410 140 0 T; 0 U; 1 Other;

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Best Local S
Matches 92
                                          The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A-s sodium channel
                                                                                                                                                                                                                                     Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                   Kanazawa I,
                                                                                                                                                                                                                                                                                                                                                                                                                23-MAY-2000; 2000JP-00152085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000; 2000WO-JP004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200190355-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL42750;
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                                                                                                                                                                                                                                                                                                                                                                                   (NISC+) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; n nervous system; chromosome 3p23-21.3; excitatory cell; development; familial hyperglycaemia; QT extending syndrome type
                                                                                                                                                                                                                                                                                                                      2002-393394/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
                                                                                                                                                                                                       7; Page 55-70; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endplate disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sodium channel subunit SCN12A-s coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA 2445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                  Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
200. .4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human sodium channel subunit SCN12A-s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%;
96.8%;
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Pred. No. 2.8e-19;
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Sequence

5728

BP; 1637 A;

1241 C;

1199 <u>ი</u>

1650

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RESULT 5
AAP301011
ID AAP310101
AAP301011
AAP30101
AAP30101
AAP30101
AAP30
AAP
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                       The present sequence is that of cDNA encoding a novel human tetrodotoxin CC resistant sodium channel, termed NaN (see AAB20121). The cDNA was CC isolated from a human dorsal root ganglia tissue cDNA library by PCR cmplification (see also AAF30122-23). NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium courrent. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres. TTX-R sodium CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic CC uses in relation to acute and/or chronic pain pathologies. A claimed CC method of treating pain, paraesthesia and/or hyperexcitability phenomena cin a human or animal subject involves administering an agent that alters codium current flow through NaN channels, or which modulates codium current flow through NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct CC isorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, cc and in the recombinant production of NaN polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Si
Matches .92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 11A; 162pp; English.
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96.8%;
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Pred. No. 3
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The present invention describes an expression vector comprising a nucleic card sequence that encodes a mammalian Na v 1.9 sodium channel protein or CC its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected CC from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; CC (2) a method of making a cell or cell line that produces a Na v 1.9 CC sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell cunder conditions that allow expression vector; and (b) culturing the cell comproduce a sodium current into the transfected cell; (3) a method of CC exposing the cell or cell line produced by the method to the agent; and CC (b) measuring sodium current following exposure to the agent, where an CC comprising the level of sodium current in a cell by: (a) calteration in the level of sodium current in a cell; and (4) a recombinant ccell comprising the expression vector. The expression vectors are useful
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Best Local
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                                                                                                                                                                                                                                                                                                                       Expression vector useful for stable cloning and expression of Navl.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Navl.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron
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                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3; 125pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "Na v 1.9 sodium channel protein"
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN2A; human nervous system; chromosome 3p23-21.3; excitatory cell; drug development; familial hyperglycaemia; QT extending syndrome type 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 200. .5575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Human sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sodium channel subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.0%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No. 3.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit; SCN12A; SCN12A-s; SCN8A; 3p23-21.3; excitatory cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 U; 0 Other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCN12A"
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The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q3.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A sodium channel subunit

Sodium channel alpha subunits SCN12A and SCN8A of human nervous s together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.

system

WPI;

2002-393394/42

23-MAY-2000;

2000JP-00152085

(NISC-)

JAPAN SCI & TECHNOLOGY CORP

Jeong

11-JUL-2000; 2000WO-JP004629

Claim 6; Page 29-46; 118pp; Japanese.

χğ

Sequence

6528

BP; 1842 A; 1446 C; 1410 G; 1830

T; 0 U; 0 Other; Length 6528;

Query Match Best Local Similarity

42.0%; 96.8%;

Score 90.2; DB 6; Pred. No. 3.4e-19;

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RESULT 8
AAX87601
ID AAX8
AC AAX8
AC AAX8
DT 26-C
DE MOU!
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                            This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat NaN-based primers (see
                                                                                                                                                                                                                                                                                                New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-1999
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                                                                                                                                                                                                                  Claim 1; Fig 7A1-3; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-479168/40.
P-PSDB; AAY06597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYYA ) UNIV YALE.
  AAX87618-19). Rat,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAGTCTGATGTTACCAGTATACCTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               channel; ion transport; mouse;
a; hyperexcitability; therapy; {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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98US-0109402P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "these bases represent nucleotides missing fithe sequence given in Fig 7 of the specification." nucleotides are included to maintain the nucleotide numbering given in the specification for this DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numbering given 
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= b
  mouse and human NaN nucleic acids (see AAX87600-02)
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Scnlla gene;
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ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The gene encoding NaN has been named Scnlla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; paraesthesia; hyperexcitability; analgesic; vaccine; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NAN, methods for identifying agents that modulate NAN channel activity or NAN channel mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse sodium channel NaN cDNA.
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                                                                                                                                                              WPI; 2001-103147/11
                                                                                                                                                                                                               Dib-Hajj S, Waxman
                                                                                                                                                                                                                                                                                                                         16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000; 2000WO-US019342
                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001.
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5789. .
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Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.

AAB20124.

Example 3; Fig 7A; 162pp; English

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RESULT 10
ADD32195
ID ADD32
XX ADD32
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful the protein and the face of the sensory neurons and the face of the sensory neurons 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, diagnosis of disease, and in the recombinant production of NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of cDNA encoding a novel mouse tetrodotoxin resistant sodium channel, termed NaN (see AAB20124). The cDNA was isolated from trigeminal ganglia cDNA using primers (see AAF30100-21) based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN (see AAB20121). The gene encoding NaN, termed Scnlla, is located on mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, indorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in
                                                                                                                                                 20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                        20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron; mouse; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD32195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD32195 standard; cDNA; 5822 BP.
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                                                          (TRAN-) TRANSMOLECULAR INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.0%;
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Pred. No. 4.8e-05;
0; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                ADD32209
                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   competitions that allow expression vector; and (b) culturing the cell conder conditions that allow expression of Na v 1.9 sodium channel protein conditions that allow expression of Na v 1.9 sodium channel protein conditions that allow expression of Na v 1.9 sodium channel protein conditions that allow expression of Na v 1.9 sodium channel protein conditions a sodium current into the transfected cell; (3) a method of conditions current into the area of conditions current in a cell by: (a) capable of modulating sodium current in a cell; and (4) a recombinant comprising the expression vector. The expression vectors are useful conditions and protein levels, and for producing sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a mouse Na v 1.9 sodium channel protein, which consider the exemplification of the Na v 1.9 sodium channel protein, which consider the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector useful for stable cloning and expression of Navl.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Navl.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gonda MA,
                                                                                                              Rattus norvegicus.
                                                                                                                                                                                                          Rat Na v 1.9
                                                                                                                                                                                                                                                15-JAN-2004
                                                                                                                                                                                                                                                                                        ADD32209;
                                                                                                                                                                                                                                                                                                                              ADD32209 standard; cDNA; 5298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTCAGTT 3028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTACGCTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGAAATTTACAGAAAAACAGTTTCCCCCCAAAAGCAACCAGATCGATGCTTTCCCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                          sodium channel protein encoding cDNA SEQ ID NO:19.
                                                                                                                                                                                                                                                (first entry)
                                                                      Location/Qualifiers
                                                        . 5298
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Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                              ВÞ
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                                                                                                                                                      neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5822;
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                                                                                                                                                    rat; gene; ss.
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/\*tag= a /product= "Na v 1.9 sodium channel protein"

/\*tag=

WO2003080570-A2

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RESULT 12
AAX60244
ID AAX60
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AC AAX60
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AC AAX60
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DT 11-AU
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DB Stabi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of exposing the cell or cell line produced by the method to the agent; and (b) massuring sodium current following exposure to the agent; and capable of modulating sodium current is indicative of an agent capable of modulating sodium current is indicative of an agent capable of modulating sodium current is indicative are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a rat Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
             Stabilised cDNA encoding type 5 sodium channel protein designated PN5
                                                     11-AUG-1999
                                                                                        AAX60244;
                                                                                                                             AAX60244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2002; 2002US-0365550P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; SEQ ID NO 19; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
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                                                                                                                                                                                                                                                                                             AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT
                                                                                                                           standard; cDNA; 5334 BP
                                                                                                                                                                                                                                                        G 201
                                                                                                                                                                                                                                                                                                                               TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCAGCGATTTTTCGTACCAACG 200
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                                                     (first entry)
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AAX87600
ID AAX87
XX AAX87
AC AAX87
AC AAX87
AC AAX87
COT 26-OC
XX Rat 8
XX NaN;
KW PAIR8
XX NAN;
KW PAIR8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodocoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy; neuropathic pain; migraine; headache; ss.
                                                                                                            NaN; sodium channel; ion transport; rat; dorsal root ganglia; pain; paraesthesia; hyperexcitability; therapy; Scnlla gene; ss.
            misc_feature
                                                                                  Rattus
                                                                                                                                                   Rat sodium channel NaN cDNA
                                                                                                                                                                               26-OCT-1999
                                                                                                                                                                                                         AAX87600;
                                                                                                                                                                                                                                     AAX87600 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Fig 5A-E; 90pp; French.
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                                                                                                                                                                                                                                                                                                                                                               2962 TTAGAAATTTÄCAGAAAACAGTTTCCCCCAAAAAAGCAGCCAGATAGATGCTTTCCCAAGG
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5551. .
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Pred. No. 0.00016;
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RESULT 14
AAF30102
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AC AAF30
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                  30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of an isolated nucleic acid which encodes the rat NaN channel (see AAY06596), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from Sprague-Dawley rat DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                    AAF30102;
                                                                                 AAF30102 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                  (first entry)
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98US-0109402P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence"
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                                                                                  cDNA; 5875
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Pred. No. 0.00016;
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Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                          Rat sodium channel NaN cDNA.
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CDS Location/Qualifiers

Rattus norvegicus.

WO200105831-A1

25-JAN-2001.

14-JUL-2000; 2000WO-US019342.

16-JUL-1999; 99US-00354147

(UYYA ) UNIV YALE.

Dib-Hajj S,

P-PSDB; AAB20122, AAB20123 2001-103147/11

Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.

Example 1; Fig 1; 162pp; English.

CC isolated from a dorsal root ganglia tissue cDNA library by PCR complification using generic primers (from conserved resions of a-subunit conditions of a subunit condition of a subunit conditions of a subunit condition of a subunit conditions of a subunit conditions of a subunit condition of a subunit conditions of a subunit condi The present sequence is that of cDNA encoding a novel rat tetrodotoxin resistant sodium channel, termed NaN (see AAB20122). The cDNA was

Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;

Matches Query Match

Local

Similarity

21.3%;

DB 4;

Length 5875; Indels

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0

Conservative

0; Mismatches Score 45.8; DB 4; Pred. No. 0.00016;

Ş 맑 S 밁 8 2919 2979 201 81 G 201 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCAGCGATTTTTCGTACCAACG AGAAGTCTGACGCAGTGAGCATGCTCTCGGAATGCAGCACAATTGACCTGAATGATATCT 3038 2978 140 200

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3039

G 3039

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RESULT 15
AAZ21480
ID AAZ21480
ID AAZ21480
AC AAZ21
XX AZ21
XX Senso
XX Senso
XX Volta
XX Volta
XX Volta
XX Volta
XX ISAN
PT CDS
PT CDS
PT CDS
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Matches | 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes rat sensory neurone specific 2a (SNS-2a). SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grose pT, Hick CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5897 BP; 1474 A; 1471 C; 1435 G; 1517 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 52-58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-562112/47.
P-PSDB; AAY41668.
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ilarity 61.2%;
Conservative
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Pred. No. 0.00016;
0; Mismatches 47; Indels
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Result
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Gapop 10.0 , Gapext 1.0
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L: /cgn2_6/ptodata/1/pubpna/US07_
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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  5 US-10-388-470-6
US-10-388-470-1
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US-10-027-632-241204
US-10-027-632-221451
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              Sequence 221452,
Sequence 6480, Ap
Sequence 91590, A
Sequence 91591, A
Sequence 317742,
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Sequence 41, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 273499,
Sequence 2, Appli
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## ALIGNMENTS

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Sequence 6, Application US/10388470

Publication No. US20030228662A1

GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
FILE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT PILLING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILLING DATE: 1998-01-29
PRIOR FILLING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US/09/2008
PRIOR APPLICATION NUMBER: US/09/2008
PRIOR APPLICATION NUMBER: PCT/US/99/02008
PRIOR APPLICATION NUMBER: PCT/US/99/02008
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US-10-388-470-6
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Query Match
Best Local Similarity
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                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
FEATURE:
NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: y = c or t. Xaa at amino acid i
OTHER INFORMATION: Leu.
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  42.0%;
96.8%;
  Score 90.2; DB 15; Pred. No. 5.2e-20;
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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US/06/109,402
PRIOR APPLICATION NUMBER: PCT/US/99/02008
PRIOR APPLICATION NUMBER: PCT/US/99/02008
PRIOR APPLICATION NUMBER: PCT/US/99/02008
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                       Sequence 4, Application US/10388470 Publication No. US20030228662A1 GENERAL INFORMATION:
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SEQ ID NO 41
LENGTH: 5860
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Best Local Similarity
                                                           APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REFERNCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
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TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
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APPLICANT: Waxman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/0200
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence
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Pred. No. 6.4e-20;
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US-10-388-470-1
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                                                                         US-10-388-470-1
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(5313)
Matches
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Maxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
CURRENT FILING DATE: 2003-03-17
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NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2
                                                                                NAME/KEY: unsure
LOCATION: (1996)..(4042)
OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.
                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (41)..(53
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rattus norvegicus
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ION: cDNA sequence for rat NaN
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Pred. No. 2.9e-05;
Score 45.8; DB 15;
Pred. No. 0.0001;
0; Mismatches 47;
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                 Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des
FILE REFERENCE: E01/1208/WO
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SEQ ID NO 273499
LENGTH: 651
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Best Local Similarity
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TYPE: DNA
ORGANISM: Human
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 2000-03-29
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CURRENT APPLICATION NUMBER: US/10/312,841
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APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-241203
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US-10-027-632-241203/c
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Publication No. US20030204075A9
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NUMBER OF SEQ ID NOS:
SEQ ID NO 1
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SEQ ID NO 241203
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Best Local
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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NAME/KEY: unsure
LOCATION: (3294164)
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                                                                                                                                                                                                                                          Local Similarity
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126 ATCTTCAGGATGGCTTTGGATGGTTACCTG 155
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                                                                                                                                          435 ATTCTGCAACTCACAATTTCTTTTTTCAAAATAGTTTTTGGGAAAAGTTTTACACTTAGT
                                                                                                  66 TITGITCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTG 125
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Pred. No. 17;
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                                                                                                                                                                                                                                                             Length 536;
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315 CTTTGAGGTTAGATTTTATTGGTAGCCAG 286

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US-10-027-632-241204/c
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US-10-027-632-241204
                  PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SEQ ID NO 241204
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 221451, Application US/10027632 Publication No. US20030204075A9
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT APPLICATION NUMBER: US/10/027,632
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PRIOR FILING DATE: 2000-02-24
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NUMBER: US 60/167,363
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Pred. No. 0.7;
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US-10-027-632-221451
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PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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Best Local (
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                           LENGTH: 586
TYPE: DNA
ORGANISM: Human
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66 TITGTICTGAIGTGCAGAAGTCTGAIGTIACCAGTAIACTAICAGAATGTAGCACCATTG
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                                                                                                                                         77; Conservative
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77; Conservative
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                                                                                                 AATGAGAAACTCCGTACTACTATGGTGAAAGAAGGTCTTAGTAAAAGGCACCCCCTTCCT 65
                                                            ATTCTGCAACTCACAATTTCTTTTTTCAAAATAGTTTTTGGGAAAAGTTTTACACTTAGT
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51.3%;
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                                                                                                                                       Score 33.2; DB 15;
Pred. No. 0.73;
0; Mismatches 73;
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FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 6480
LENGTH: 1581
RESULT 12 |
US-10-027-632-91590
· Sequence 91590, Application US/10027632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-198-846-6480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: HOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1140, 1153, 1159, 1216, 1231, 1236, 1249, 1264, 1276, 1280,
LOCATION: 1301, 1302, 1319, 1333, 1342, 1375, 1380, 1382, 1419, 1422,
LOCATION: 1424, 1434, 1438, 1448, 1450, 1492, 1535, 1556, 1567, 1571,
LOCATION: 1573, 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 173, 175, 183, 185, 189, 195, LOCATION: 173, 175, 183, 185, 189, 195, LOCATION: 264, 265, 268, 275, 276, 307, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
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                                                                                                                                                                                                              TTTTTTTCCTTTCCAAAAGAGGCCTTTAAATTTNCTTTTTTNCCTTNGGGGTGAAAGGGN 981
                                                                                                                                                                                                                                                                                                                              AAGGTCTTAGTAAAAGGCACCCCCTTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTAC 96
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                                                                                                                                   TTTTTCCCCCCAAAAAAAATTNCCCCCAATTTTTNGGCCCCAAAGG 1026
                                                                                                                                                                        GATGGTTCCCAAAGAAAATTTCCAGCGATTTTCGTACCAACGG 201
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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505,
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197,
325,
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787, 805,
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199,
337,
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218,
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560,
871,
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620
895
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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; ORGANISM: Human
US-10-027-632-91590
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PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PRILING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                 PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows
SEQ ID NO 91591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 91591, Application US/10027632 Publication No. US20030204075A9
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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ENGTH: 539
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                                                      Version 4.0
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Pred. No. 1
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US-10-027-632-317743
, Sequence 317743, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,318
PRIOR APPLICATION NUMBER: US 60/187,363
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TYPE: DNA
ORGANISM: Human
S-10-027-632-317742
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 317742
LENGTH: 539
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/146,002
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nes 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 58.3
nes 56; Conservative
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APPLICATION NUMBER: US 60/156,358
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; ORGANISM: Human
US-10-027-632-317743
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                             ENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR APPLICATION NUMBER: US 60/167,363
OR APPLICATION NUMBER: US 60/156,358
OR APPLICATION NUMBER: US 60/156,358
OR APPLICATION NUMBER: US 60/156,358
OR FILING DATE: 1999-09-28
                                                                                                                                                                                       Local Similarity
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147
                                       86 TCTGATGTTACCAGTATACTATCAGAATGTAGCACC 121
                                                                              87 TATGTGTACAGAATGTGTTAGTATAACACATATATTTCCTTGTTCTGTCAGGTGGGAGAG 146
                                                                                                                      56; Conservative
CCTAAAAGCAGTAATATACCAATAGTAACAAGCACC
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                                                                                                                                                                                     14.9%;
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                     Score 32; DB
Pred. No. 1.8;
                                                                                                                                                                                                           15; Length 539;
                                                                                                                                                                   40;
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Search completed: March 23, 2004, 05:12:00 Job time: 217.682 secs

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Minimum DB
Maximum DB
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Perfect score:
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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215
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/cgn2_6/ptodata/2/pna/
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gn2_6/ptodata/2/pna/USO7_COMB.seq:*
gn2_6/ptodata/2/pna/USO82_COMB.seq:*
gn2_6/ptodata/2/pna/USO83_COMB.seq:*
gn2_6/ptodata/2/pna/USO83_COMB.seq:*
gn2_6/ptodata/2/pna/USO83_COMB.seq:*
gn2_6/ptodata/2/pna/USO85_COMB.seq:*
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45. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 46. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 47. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 48. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 48. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 49. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 59. / cgm2 - 6/ptodata / 2/pna/USIONB_COMB. seq: 69. / cgm2 - 6/ptodata / 2/pna/USIONB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-646-224A-11

Sequence 11, Application US/09646224A
GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome PLC
APPLICANT: Tate, Simon N
APPLICANT: Grose, David T
APPLICANT: Hicks, Caroline A
TITLE OF INVENTION: Ion Channels
FILE REFERENCE: PG3432
CURRENT APPLICATION NUMBER: US/09/646,224A;
CURRENT FILING DATE: 2000-09-14;
PRIOR APPLICATION NUMBER: GB 9805793.8;
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 35;
SOFTWARE: Patentin Ver. 2.1;
SEQ ID NO 11;
LENGTH: 215
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No.
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PCT-US90-19342-6
PCT-US90-2036-6
10 US-10-38-470-6
10 US-10-38-470-6
10 US-60-453-050-2171
10 US-60-453-135-2171
17 US-10-219-0518-910
18 US-10-296-130-3
19 US-10-388-470-41
19 US-10-388-470-41
19 US-10-388-470-41
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2 US-10-296-130-1
05 US-60-485-101-251
02 US-60-485-101-251
02 US-60-453-050-33591
03 US-60-466-412-33591
04 US-10-180-19342-4
05 US-10-180-19342-4
06 US-10-388-470-4
07 US-10-388-470-4
07 US-10-388-470-4
08 US-10-180-934-1
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7 US-60-213-846-31
7 US-60-213-846-334
7 US-60-213-846-335
7 US-60-213-846-335
7 US-60-213-846-337
7 US-60-213-846-337
7 US-60-213-846-337
7 US-60-213-846-339
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7 US-60-466-412-15225
9 US-60-466-412-152339
9 US-60-243-866-412-152339
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Sequence 22, App
Sequence 334, App
Sequence 335, App
Sequence 336, App
Sequence 337, App
Sequence 337, App
Sequence 338, App
Sequence 339, App
Sequence 15259,
Sequence 15259,
Sequence 15259,
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Sequence 7171, Ap
Sequence 2171, Ap
Sequence 2171, Ap
Sequence 3195, A
Sequence 3191, Appli
Sequence 41, Appli
Sequence 31, Appli
Sequence 33591, A
Sequence 3591, A
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Sequence 4, Appli
Sequence 4, Appli
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Best Local Similarity
Matches 215; Conserv
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APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000163
CURRENT APPLICATION NUMBER: US/60/169,841
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 2910
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 129
LENGTH: 437
TYPE: DNA
RORANLSM: Human
US-60-169-841-129
Sequence 31, Application US/60213846
; Sequence 31, Application US/60213846
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
; CURRENT APPLICATION NUMBER: US/60/213,846
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 129, Application US/60169841 GENERAL INFORMATION:
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SEQ ID NO 31 LENGTH: 30565

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ORGANISM: HUMAN FEATURE:

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Sequence 334, Application:
Sequence 334, Application:
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NU USES THEREOF
FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 334
LENGTH: 32768
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US-60-213-846-335
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Sequence 335, Application US/60213846
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.3
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER:INFORMATION: n = A,T,C or
-60-213-846-334
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LOCATION: (1)...(30565)
OTHER INFORMATION: n = A,T,C or
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Similarity 98.3%;
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98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 170.2; DB 77; Length 32768; Pred. No. 3e-42;
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Pred. No. 2.9e-42;
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US-60-213-846-336

(SEQUENCE 336, Application US/60213846
(SENERAL INFORMATION:
(APPLICANT: Beasley, Ellen
(APPLICANT: BEASLEY, Ellen
(APPLICANT: BEASLEY, Ellen
(APPLICANT: DE INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
(TITLE OF INVENTION: AND USES THEREOF
(APPLICANT)
(FILE REFERENCE: CL000703
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 336
LENGTH: 32768
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                                                                                                                                                                                                                                                                Query Match
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ORGANISM: HUMAN
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
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                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C
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Local Similarity 98.3%;
nes 172; Conservative
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                       121 CATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCCAAAGAAAAA 175
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                                                                                          TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC 120
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CATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAAAGCAA 24591
                                                                        TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC
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98.3%;
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                                                                                                                                                                                                                        Score 170.2; DB Pred. No. 3e-42; 0; Mismatches
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RESULT 7 US-60-213-846-337

Sequence 337, Application US/60213846
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen

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US-60-213-846-338

Sequence 338, Application US/60213846

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISCLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: OCCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 32768
                                                                                                                                   Query Match
Best Local :
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Best Local Similarity
                                                                                                               Matches 172;
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/60/213,846 CURRENT FILING DATE: 2000-06-23
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                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (1)...(32768)
OTHER INFORMATION: n = A,T,C
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ORGANISM: HUMAN
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                                                                                                                 Local Similarity 98.3
hes 172; Conservative
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TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC 120
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98.3%;
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                                                                                                               Score 170.2; DB Pred. No. 3e-42; O; Mismatches
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                                                                                                                                                   DB 77;
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Query Match Best Local Similarity

79.0**%**; 97.7**%**;

Pred. No. 5.9e-42;

DB 103;

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US-60-466-412-84151
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US-60-213-846-339
                                  US-60-466-412-84151
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GENERAL INFORMATION:
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                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 84151
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Best Local Similarity
                                                APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DE:
TILE REFERENCE: CL001466
CURRENT APPLICATION UNUBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
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TYPE: DNA
ORGANISM: HUMAN
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NAME/KEY: misc_feature
LOCATION: (1)...(32768)
OTHER INFORMATION: n =
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Length 115159;
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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOP
FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1109
LENGTH: 3194
TYPE: DNA
ORGANISM: HUMAN
US-60-213-846-1109
                                                                                                                                                                                                                                                                                                                 RESULT 12
US-60-213-846-1109
Sequence 1109, Applic
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-60-466-412-152259
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US-60-466-412-152259
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Best Local Similarity
Matches 163; Conserv
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APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01466
CURRENT [APPLICATION NUMBER: US/60/466,412
CURRENT [FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 152259
LENGTH: 201
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 Query Match
Best Local Similarity 100.0%;
Matches 118; Conservative
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99.4%;
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0; Mismatches
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                  Score 118; DB 77;
Pred. No. 4.6e-26;
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US-60-213-846-1412
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CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 152339
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
                                                                                                                                                                                                                                                                                              SEQ ID NO 1412
LENGTH: 3163
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APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
                                                                                                                                                           Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1412,
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                                                                                                                                                                                                                                                      LENGTH: 3163
TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DEFILE REFERENCE: CL001466
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
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Similarity 100.0%; P
                                                                                                                                                                            Similarity
                       AGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
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                                                                           CTGAACAACAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTC
                                                                                                               CTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/60213846
                                                                                                                                                         Conservative
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                                                                                                                                                                          43.2%;
                                                                                                                                                       Score 92.8; DB 77
Pred. No. 4.4e-18;
0; Mismatches 7
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Pred. No.
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Sequence 6 Application PC/TUS0019342

Sequence 6 Application PC/TUS0019342

CENERAL INFORMATION:

APPLICANT: Vale University

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-504-02-W0

CURRENT APPLICATION NUMBER: PCT/US00/19342

CURRENT APPLICATION NUMBER: PCT/US00/19342

CURRENT APPLICATION NUMBER: US 09/354,147

PRIOR FILING DATE: 1999-07-16

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 3701

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3699)

COTHER INFORMATION: partial human NaN cDNA sequence
NAME/KEY: unsure
LOCATION: (922)

COTHER INFORMATION: y = c or t

PCT-US00-19342-6
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PCT-US00-19342-6
Search completed: March 23, 2004, 04:00:02 Job time : 1638.26 secs
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                                                                                                                                                                                                                             2351 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 2410
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Perfect score:
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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| Cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| Cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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6 US-10-767-771-13578
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US-10-796-280-12202
US-09-969-034-2460
US-09-969-034-2460
US-09-548-091-2114
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Sequence 10599, A
Sequence 13578, A
Sequence 13578, A
Sequence 13578, A
Sequence 2460, Ap
Sequence 2460, Ap
Sequence 2104, Ap
Sequence 2114, Ap
Sequence 2114, Ap
Sequence 2144, Ap
Sequence 2155, Ap
Sequence 2159, Ap
Sequence 2179, Ap
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Sequence 2187, Ap
Sequence 1013, App
Sequence 1015, App
Sequence 101, App
Sequence 101, App
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Sequence 97, Appl
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence
7028, Ap	2757, Ap	2756, Ap	17704, A	59211, A	57054, A	18156, A	15999, A	10648, A	2987, Ap	10854, A	41, Appl	3063, Ap	5629, Ap	Sequence 10805, A	5620, Ap	102, App	99, Appl	106, App

## ALIGNMENTS

RESULT 1 US-10-767-471-10599/c

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RESULT 2
US-10-767-471-10805/c
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
FILE REFERENCE: CLOO1505
CURRENT APPLICATION UNMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
                                                                                                      SEQ ID NO 10805
LENGTH: 1790242
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                                                                                                                                                           NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
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TYPE: DNA
                           ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature
                                                                                   TYPE: DNA
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; LOCATION: (1)...(1790242) ; OTHER INFORMATION: n = A,T,C US-10-767-471-10805

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or insertion/deletion polymorphism (see

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21 (53555)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 13578 LENGTH: 1051 TYPE: DNA ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13578, Application US/10767701 GENERAL INFORMATION:
                                                                                                                                                              Sequence 6590, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalio, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                              APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(33535)8
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                    TTCGTA 194
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Pred. No. 15;
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Pred. No.
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; OTHER INFORMATION: Clone ID:
US-10-767-701-6590
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US-10-796-280-12202
                                                                                                                                                                                                                                              US-09-969-034-2460
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                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(303523)
OTHER INFORMATION: n = i
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US
FILE REFERENCE: CL001510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
                                                                                                                  APPLICANT:
                                                                                                                                                 APPLICANT:
                                                                                                                                                                               APPLICANT: Burgess, Chris
                                                                                    APPLICANT:
                                                                                                    APPLICANT:
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                                                      OF INVENTION:
P. Dwivedi, roca.
T: Molino, Gary A.
T: Molino, Gary A.
T: Thiagalingam, Arunthathi
NT: Lewis, Marcia E.
PRINTENTION: Nucleic Acid Sequences Differentially
RESERVATION: Expressed in Cancer Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 GCGATTTTTCGTACCAACGGTTACGCTT 209
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                                                                                                                                                                                                                                                                                                                                                                                                          85 GTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCTTTGG
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                                                                                                                                                                                                                                                                                                              TTCACTCCATCTGAAATCTACTAAAACAGTATTTGGAATTATT 224313
                                                                                                                                                                                                                                                                                                                                                                            TGTTGGTTTTAAAACAATAATAAGAAAAAAAACAAACCATAATTCATGAAGAAGTATCTGA
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                                                                                                                                                                                                                                                                                                                                            ATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCAGCGATT 187
                                                                                                                                                 Carroll, Eddie III
Catino, Theodore J.
                                                                                                                                                                                                                               Application US/09969034
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58.0%;
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Pred. No. 34;
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Pred. No. 3
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TYPE: DNA
TYPE: DNA
GRANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 217, 267, 269, 271, 2
OTHER INFORMATION: n = A,T,C or
US-09-969-034-2460
RESULT 8 |
US-60-548-091-2104
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; Sequence 20110, Application US/10793479
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2460
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 20110
LENGTH: 164
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.USZ. REG

CURRENT APPLICATION NUMBER: US/10/793,479

CURRENT FILING DATE: 2004-03-03
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                                                                                                                                                                                                                                                                                                                                                                        PEATURE: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                      GATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGG 161
                                                                                                                                                                                                            TTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATT 124
                                                                                                      TTCGAAAAGCATTATTTTGTTTTGTTTTCTGGGATGG 37
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             Application US/60548091
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55.7%;
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Pred. No. 3
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LENGTH: 201
TYPE: DNA
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2104
                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity 51.2%;
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT FAPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
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ORGANISM: Homo sapiens
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                                                                                                          165
                                                                                                                                                                   105 TATCAGAATGTAGCACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTC 164
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                                                                                                                                              97
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                                                                                                          CCAAAGAAA 173
                                                                         TTTATAAAA 165
                                                                                                                                              TACAYGTCATTTTTACCAATGATTTTCAGGTGACCTGGGCTAAGTCATTTAAACTGGGTC 156
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51.2%;
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Pred. No. 3.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                          Score 28.2; D
Pred. No. 3.7;
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Sequence 2125, Application US/60548091 GENERAL INFORMATION: APPLICANT: CARGILL, Michele et al.

Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH

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CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2125
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-548-091-2125
              US-60-548-091-2155
Sequence 2155, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001506
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US-60-548-091-2142
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; ORGANISM: Homo
US-60-548-091-2142
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPH:
TITLE OF INVENTION: STROKE, METHODS (FILE REFERENCE: CL001506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2142
LENGTH: 201
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Best Local
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Best Local Similarity
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FILE REFERENCE: CLO
CURRENT APPLICATION
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STROKE, METHODS OF DETECTION AND USES THEREOF
NUMBER: US/60/548,091
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Pred. No. 3.7;
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US-60-548-091-2179
; Sequence 2179, Application US/60548091
; GENERAL INCORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USE
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FABLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSEQ for Windows Version 4.0
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US-60-548-091-2164
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Matches
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LENGTH: 201
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Best Local (
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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SOFTWARE: FastSEQ for Windows Version
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 3.7;
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US-60-548-091-2187
US-60-548-091-2187
; Sequence 2187, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 2187
Search completed: March 23, 2004, 04:48:14 Job time : 3/2.461 secs
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; LENGTH: 201
; TYPE: DA
; ORGANISM: Homo sapiens
US-60-548-091-2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-2187
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Best Local Similarity 51.2%;
Matches 66; Conservative
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Best Local Similarity
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    nucleic search, using sw model

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ALIGNMENTS

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Ay404476
Pan troglodytes SCN11A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
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ON Ay404476
ON Ay404476.1 GI:39760453
GSS.
Be pan troglodytes (chimpanzee)
Pan troglodytes (chimpanzee)
Pan troglodytes (Chimpanzee)
Charyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
ENCE 1 (bases 1 to 3772)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Farenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
LE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Science 302 (5652), 1960-1963 (2003)
ENCE 2 (bases 1 to 3772)
ENCE 2 (bases 1 to 3772)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ford, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
LE Direct Submission

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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,
Clark,A.G., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4614)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (16-NOV-2003) Celera Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 302 (5652), 1960-1963 (2003)
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                                                 /gene="SCN11A"
/locus_tag="HCM1903"
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                                                                                                                                                                                                                                                                                                                 81 AGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCT 140
                                                                                 wlm96.jk0005.e10 wlm96 Triticum aestivum wlm96.jk0005.e10 5' end, mRNA sequence. CA682659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4556)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 4556)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                   EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene trios
Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus SCN11A gene,
               Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was made by sequencing them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
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Eukaryota;
                                                                 CA682659.1
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                                                                                                                                                                                                                                                         TTGGATGGTTACCTGAGATGGTTCCCAAAGAAAATTTCCAGCGATTTTTCGTACCAACG
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SCN11A"
/locus_tag="HCM1903"
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Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                   GI:25268432
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Pred. No. 0.0016;
0; Mismatches 46;
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VIRTUAL
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RESULT 5
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JOURNAL
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JOURNAL
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Best Local (
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                   Bource
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tingey,S.V., Powell,W., Wolters,P.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                     Maize Genomics Consortium Unpublished (2003)
Other_GSSs: PUFKQ57TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 931)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
CG117098
CG117098.1 GI:34000535
GSS.
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Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG117098 931 bp
PUFKQ57TB ZM_0.6_1.0_KB Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crop Genetics
E. I. DuPont de Nemours and Company
                                                                                   Email: whitelaw@tigr.org
                                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                                                                                                         Bennetzen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13
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Pooldeae; Triticeae; Triticum.
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                                                   primer: TR
ss: sheared ends.
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                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db xref="taxon:4565"
/clone="wlm96.pk0005.e10"
/tissue_type="leaf"
/clone_lib="wlm96"
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/cultivar="Stephens"
/organism="Zea mays"
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54.3%;
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Pred. No. 1.
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                                                                                                                                     Rockville,
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                                                                                                                                     20850,
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ZMMBTa0672I17,
                                                                                                                                       USA
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Best Local S
Matches 76
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CG117099.1
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                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Other_GSSs: PUFKQ57TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUFKQ57TD ZM_0.6_1.0_KB
                                                                                                                                                                                                                                                                                              Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                 Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                            Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitelaw, C.A., Quackenbush, J., Resnick, A., Fraser, C.M., Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
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                                                                                                                                                                                                                                                                               Seq primer: TF
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                                                                    Similarity
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                        TTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCAC 120
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                                                      Conservative
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                                                                                                                     /clone="ZMMBTa0672117"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="2MMBTa0672117"
/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                       Location/Qualifiers
1. .948
                                                                                                                                                                             /strain="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                        /organism="Zea mays"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="B73"
/db_xref="taxon:4577"
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                                                                   16.9%;
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                                                    Score 36.4; D
Pred. No. 1.6;
0; Mismatches
                                                      <u>.</u>
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68 TGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTAGCACCATTGAT 127
                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fizames, C., Fischer, C., Bouneau, L., Blitaut, A., Querter, C., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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GSS; genome survey sequence.
Tetraodon nigroviridis
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                                                                            Direct Submission
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                                        116 ACATGAGATCGAAAATTAACTGAGATAGTTAACGGAGAAGAATCTGAAGTGAATCAACT 57
                                                                           133 GGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAATTTCCAGCGATTTTTCG 192
    193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Project. All sequences in the project were assembled annotated. This entry and all the assembled sequences can be in the following URL http://bioinfo.iq.usp.br/schisto/plate: MSI-0119U-D304 row: 3 column: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de
Av. Prof. Lineu Prestes 748 sala 1200,
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This sequence was derived from the FAPESP Schistosoma mansoni
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1 (bases 1 to 380)
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    TACCAACGGTT 203
                                                                                                                          TGAAATTAAGAGGTTTGATCGGGCTGCTAGATTCGAGGAAGATCGCGCAGTTGGTTTAGA
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/note="Vector:
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/lab_host="in vitro culture"
/clone_lib="MS1-0119"
                                                                                                                                                                                                                                                                                                                                                                                                                     clone="MS1-0119U-D304-C03.B"
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Best Local S
Matches | 51
                                                                                                         TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angen EST Program.
Angen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 CACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norvegicus cDNA clone nrhy5-00295-c5 5', mRNA linear EST 01-APR-2003 CB546546 GI:29430487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                              1103 bp mRNA linear ES', AGENCOURT 14097420 NIH MGC_180 Homo sapiens cDNA clone IMAGE:33378187 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

i (bases 1 to 1103)
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                  CD244233.1 GI:31004697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 00295 row: c column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 805 447-4881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amgen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGCGATTTTCGTAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAATAAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAGGCTTCGTCCTCAC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amgen Center Drive, Thousand Oaks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="nrhy5-00295-c5"
/clone lib="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; W
hypothalamus adult female Wistar rat avg. Insert size
kb fraction 6 and 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
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Pred. No. 4.9;
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REFERENCE
AUTHORS
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Best Local (
                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 GCACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 CCCTTAAATTTATTTTGATGGGCCCAAATAAACCTTTCCCAGGACCCTATNTTTATTGC 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792 GTAAAATGGGCCTTTGGAAAGGAAAGGAATGGCTCTCCCAAATGCTTTCCCAAACAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CCCCTTCCTTTTGTTCTGATGTGCAGAAGTCTGATGTTACCAGTATACTATCAGAATGTA 116
                                                                                                                                                                                                                                 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al. Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX507474 481 bp mRNA linear EST 04-SEP-DKFZp686022259_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686022259_5', mRNA sequence.

BX507474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
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                                                                                                                                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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High quality sequence stop: 505.
Location/Qualifiers
                                                                           Berlin-Charlottenburg, GERMANY;
Location/Qualifiers
                                                                                                                             This clone (DKFZp686022259) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                       German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX507474.1 GI:32040151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCCAGCGAT 186
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                                                                                                                                                                                  sequence available.
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/clone="IMAGE:30378187"
/lab_host="DH108-Ton A ( T1 and T5 phage resistances)"
/clone lib="DH108-Ton A ( T1 and T5 phage resistances)"
/clone lib="NIH McC 180"
/clone lib="NIH McC 180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT prImed and directionally cloned (EcoRV Site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
/organism="Homo sapiens"
/mol_type="mRNA"
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'mol_type="mRNA"
                                                         .481
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53.8%;
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Pred. No. 6.
                                                                                                        Email: clone@rzpd.de
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RESULT 12
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                                                                              Best Local Similarity Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 AGCACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
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                                                                                                                                                                                                                                                                                                                                                                                      No s1 sequence available.
This clone (DKFzp68600311) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dktz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
because Chemiany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 531)
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DKFZp68600311_r1 686 (synonym: hlcc3) Homo
DKFZp68600311_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiemann,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL700928.1 GI:19621461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCCAGGCCTCATCCTCACTA 167
                                       AGCACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAAA 175
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
                                                                                                                                                                                   /clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp68600311"
                                                                                                                                                                                                                                                                    /dev_stage="adult"
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                                                                                                                                                                                                                                                ab_host="DH10B"
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63.4%;
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                                                                                0
                                                                                                   Score 34; DB 9;
Pred. No. 8.4;
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                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                  30;
                                                                                                                       Length 531,
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                                                                                  Indels
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CDNA clone
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RESULT 13
CA126046/c
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DEFINITION
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AUTHORS
TITLE
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Best Local
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304
                                        154
                                                                                   364
                                                                                                                                                                      424 AAGCGGGTATGGCTTTACGAAGGCTTCTTGCTGTTGTCCTCGAAAATACTAGTATCATGC
                                                                                                                                                                                                                 34
                                                                                                                     94 TACCAGTATACTATCAGAATGTAGCACCATTGATCTTCAGGATGGCTTTGGATGGTTACC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 569)
Vettore, A. L., da Silva, F. R., Kemper, E. L. and Airuda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA126046 569 bp mRNA linear F SCRULR1042F12.g LR1 Saccharum officinarum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through the Brazilian Clone Collection Center (BCCC) http://www.bcccenter.fcav.unesp.br Plate: 042 row: F column: 12 Seq primer: T7 Promoter Primer. Location/Qualifiers
                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centro de Biologia Molecular e Engenharia (
Universidade Estadual de Campinas
Calxa Postal 6010, 13083-970, Campinas SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5', mRNA sequence.
CA126046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharum officinarum
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                                                                                 TGAGATGGTT 163
                                                                                                                                                                                                            AAGAAGGTCTTAGTAAAAGGCACCCCTTCCTTTTGTTCTGATGTGCAGAAGTCTGATGT 93
TAAGCTCGTT 295
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                            /clone lib="LR1"
/note="Organ: Leaf roll from field grown adult plants
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: Not1; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="SCRULR1042F12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Saccharum officinarum"
                                                                                                                                                                                                                                                                           15.8%;
                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                       Score 34; DB 13;
Pred. No. 8.5;
0; Mismatches 60
                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                    Length 569
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e SCRULR1042F12
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RESULT 14 CD559574/c

DEFINITION

EST 26-NOV-2003

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JOURNAL COMMENT
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                                                                                                                                                     116 AGCACCATTGATCTTCAGGATGGCTTTGGATGGTTACCTGAGATGGTTCCCAAAGAAAA 175
                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Bhat Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Plate: IRBK1 row: c column: 10 High quality sequence stop: 717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Cancer Institute / NIH
Bldg. 31 RmlOA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585642
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 785)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD559574 785 bp mRNA linear ES' AGENCOURT 14496977 NIH MGC 195 Homo sapiens cDNA clone IMAGE:6971723 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD559574.2 GI:38559021
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TTTCCAGGCCTCATCCTCACTA 142
                                                    TTTCCAGCGATTTTTCGTACCA 197
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="PH5A (TI phage-resistant)"
/clone lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
/note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
loxP-HindIII; Clones from this library have been
PCR amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq!. Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA: from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, M2 1702). For
                                                                                                                                                                                                                                                                                                                                         visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                       information on which gene each clone represents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971723"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="mixed"
                                                                                                                                                                                                                                   15.8%;
                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                      Score 34; DB 14; Length 785 Pred. No. 9;
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Search completed: March 22, Job time : 1277.46 secs

2004, 23:12:20

RESULT 15

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LOCUS
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Best Local'S
Matches 52
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                                                                           142
                                     176
                                                                                                             116 АССАССАТТСАТСТТСАССАТСССТТТССАТССТТАССТСАСАТССТТСССАЛАСАЛЛАА 175
 82
                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1837 bp
Homo sapiens HCM4347 gene, VIRTUAL
genomic survey sequence.
AY411807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1837)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene trios
Science 302 (5652); 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14671302
TTTCCAGGCCTCATCCTCACTA 61
                                   TTTCCAGCGATTTTTCGTACCA 197
                                                                           (bases 1 to 1837)
                                                                                                                                                                                                                                                                                                                                                                                  sequence was made by sequencing genomic exons and ordering based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens (human)
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                             locus_tag="HCM4347"
                                                                                                                                                                     15.8%; Score 34; DB 29; Length 1837; 63.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                     .>1837
                                                                                                                                                   0,
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear GSS 12-DEC-2003 TRANSCRIPT, partial sequence,
                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                                                                                          45 West Gude Drive,
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kejariwal, A.,
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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Maximum Match 100%
Listing first 45 summaries
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Pred
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## SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL		DEFINITION ACCESSION VERSION	RESULT 1 AX017228 LOCUS		C 444 5		C 41	40		C 36		C 33	32		0 0 228					c 21		c 18	16 17	15	13	12 .	10	wα	0 7	<b>σ</b> (		α ω (	2 1	jult No.
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JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX017228	VEGOTI
Patent: WO 9947670-A 12 23-SEP-1999;	Mammalian sodium channel proteins	Tate, S.N., Grose, D.T. and Hick, C.A.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX017228.1 GI:10042148	AX017228	Sequence 12 from Patent WO9947670.	AX017228 346 bp DNA linear PAT 07-SEP-2000		

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PF 18-MAR-1999 JF 2000536853
PF 18-MAR-1999 JF 2000536853
PR 18-MAR-1998 GB 9805793.8
PI DAVID THOMAS GROSE CAROLINE ANNE HICK, SIMON NICHOLAS TATE C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC12N1/15,
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1 (bases 1 to 346)

Grose, D.T., Hick, C.A. and Tate, S.N.
Mammalian sodium channel protein
Patent: JP 2002508941-A 11 26-MAR-2002;
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HTG.
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Kaul,R.K., Olson,M.V., Raymond,C. and
Direct Submission
Submitted (23-MAR-2002) Genome Center,
                                  Direct Submission
Direct Submission
Submitted (07-OCT-2003) Genome Center, University of Washi
Box 352145, Seattle, WA 98195, USA
On Oct 7, 2003 this sequence version replaced gi:21622736.
                                                                                                                    Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 167476)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                     Submitted (28-JUN-2002) Genome Box 352145, Seattle, WA 98195,
                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                    Box 352145, Seattle, WA 98195, U 3 (bases 1 to 167476) Kaul, R.K., Olson, M.V., Zhou, Y., Saenphimmachak, C., Phelps, K.A.,
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Kaul, R.K., Olson, M.V., Zhou, Y.,
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Pred. No. 6.7e-96;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       Center,
USA
                                                                                                                                                                                                                                                                                            Center,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                            Kibukawa,M.,
                                                                                                                                                                                                                                         James,R.A.,
Buckley,D.,
                                                                                                                                                                                                                                                                                                                                         Haugen, E.D
                                                                                                                                                                                                                                                                                                         University
                                                                       University of Washington,
                                                                                                                                                                                        University
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Kibukawa, N
                                                                                                                      Rouse, G., Wu, Z., Raymond, C. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete sequence
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                                                                                                                                                                                          of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 07-OCT-2003
                                                                                                                                                                                                                                       , Wu, Z.,
,M., Raymond, C.
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                                                                                                                                                                                                                                                                                                         Washington,
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Code: UWGC

Sequermap         Fingreint         Sequermap         Fingreint           8696         8629         2732         2741         2234         2259           6         <800         6382         6514         2067         2008           2248         2299         512         <800         5097         5007           9345         9792         449         <800         2317         2259           2016         2003         2707         2741         2813         2744           4889         4771         4809         4878         2537         2550           3455         3447         184         <800         1923         2008           245         <800         5816         5899         2486         2550           72         <800         1364         1346         4036         3992           4175         4167         999         990         2583         2550	levels above 40 are expected to have less than in 10,000 bp. Base-by-base quality values are rally visible from the GenBank flat file formate available as part of this entry's ASN.1 file.  Ence was finished as follows unless otherwise chemistry or covered by high quality data (i.e. 30); an attempt was made to resolve all sequence with the assembly was confirmed by restriction and the assembly was confirmed by restriction and the assembly was confirmed by restriction and the assembly was confirmed by restriction validation:  Validati	Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu
7181 6166 6166 8764 8764 8764 3737 3737 3711 9961 9961 8662 1565	331 2328 2038 2038 712 712 1368 1368 11620 1620 775 2583 2709 2709 2709 19834 19834 651	72 6640 4710 4710 3468 687 3049 
7213 6159 <800 8629 <800 3718 3718 9792 <800 8629	<800 2299 2003 <800 1370 <800 1560 <800 2686 2686 2686 299 <800	<800 6560 4771 3447 <800 3091 <800 <800 <800 5088 6560
3594 3172 1172 316 4023 1975 1975 1341 1341 1341 1346 3569 1229	5050 1053 1053 3231 3231 5444 1265 1265 1265 1436 1436 5528 5528 5528 5528 5528 5528 5528 552	3014 4721 727 727 179 179 1723 2078 1891 1891 1891 1891 92 92 92 93 5478
<pre>&lt;800 3639 11188 &lt;800 4039 2040 &lt;800 1346 4430 3639 1188</pre>	<pre>&lt;800 4878 1068 3264 &lt;800 5397 1128 &lt;800 11408 5397 &lt;800 2371 5089</pre>	3028 4667 745 <800 7158 2040 1188 8171 <800 3639
	953 4728 178 122 122 694 3022 4079 1294 1294 1294 2044 3725 790 4232 4232 4714	2738 2738 4704 4704 2649 2550 2550 2550 3588 6949 604
2550 <800 4223 917 <800 <800 1220 2008 <800 2744 3339	943 4629 <800 11220 <800 3007 3992 11220 2008 3544 <800 4223 <800	2744 4629 2744 2550 4862 6960 4629 3544 <800 6106

•	AUTHORS TITLE JOURNAL REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM ORGANISM	RESULT 4 AC124662 LOCUS DEFINITION ACCESSION	Qy Db 10	Ο <sub>γ</sub> 10	Qу ДЪ 10	Qу ДЬ 10	Оу ДБ 10	Query Match Best Local Matches 28						
Boukhgalter, B., Choe Cook, P., Cooke, P. Faro, S., Ferreit, Galagan, J., Gard Grand-Plerre, N., Johnson, R., Jone Lamazares, R., La Liu, G., MacLean, Matthews, C., McC, Meneus, L., Mihov Nicol, R., Norbu,		AC124662.5 HTG; HTGS MUS mUSCUI MUS mUSCUI MUS mUSCUI; Mus muscui; Eukaryota; Mammalia; I (bases	AC124662 Mus musculus IN PROGRESS : AC124662	283 TAAGATATACTTTC            105932 TAAGATATACTTTC	223 TTTTCCTGGGTTAC	163 AGAGAAAGGTGGAA           106052 AGAGAAAGGTGGAA	103 GTCCCAGTTTGAAG              6112 GTCCCAGTTTGAAG	46 TAACTTAATGGAAT	Similarity 3; Conservat				3 1	1568 1	835
galter, B. Brown, A., Camarata, J., Co, B., Choepel, Y., Colangelo, M., Cooke, P., DeArellano, K., Dewa S., Ferreira, P., FitzGerald, M., F an, J., Gardyna, S., Ginde, S., Gord Perre, N., Hagos, B., Horton, L., Dones, C., Kamar, A., Karata ares, R., Landers, T., Lehoczky, J., MacLean, C., MacConald, P., Majo aws, C., McCarthy, M., McEwan, P., Majo aws, C., McCarth	Nusbaum, C. and Lander, E. us chromosome 9, clone RP24- d to 241289) Linton, L., Nusbaum, C., Land Linton, L. Bostin V.	<b>1</b> 11	241289 bp omosome 9 clone 11 unordered pi	TAAGATATACTTTCTACCCTAAAAGCTTCTGTGACAGCCAAGATGAGCTGTAGC 	TTACCAGCCTGCCCAGTGCTT	AGACCAACAGTTCTTTTTGGG 	GAATGAAGGTACATTCTGCAG            GAATGAAGGTACATTCTGCAG	TAGAACCTTCCGGATCTAC 	73.8%; Score 255.2; DB 96.3%; Pred. No. 1e-67; ive 0; Mismatches	5401 567	1048	2033		.560 602	511
Campopiano, A. (Campopiano, A. (Callins, S. Coll) (Collins, S. Coll) (Collins, S. Goyette, M. Gayette, M. (Goyette, M. (Go	-409K22 der,E., Ali,A., Allen	CTIVEFIN. ; Vertebrata; athi; Muridae;	linear HTG 09K22 map 9, ***		TITICCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAAITTGAGGGGTAGAGAAAAGCC 	AGAGAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTCCTTAAATTGCCAAGC 	GTCCCAGTTTGAAGGAATGAAGGTACATTCTGCAGAAGAATGGGTAGAAGTTCAGTTAAC 	TAACTTAATGGAATTAGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT	9; Length 167476; 8; Indels 3;		1068 4811	2040 252	555	<800 1242	<800 253
hang, J., more, A., more, A., Dodge, S., D., Graham, L., Graham, L., JaRocque, K., JaRocque, K., Nguyen, C., Nguyen, C.,	, N.,	Euteleostomi; Murinae; Mus.	; 22-NOV-2003 SEQUENCING	336 105879	AGCC 282      AGCC 105933	AAGC 222      AAGC 105993	TAAC 162      TAAC 106053	CGCT 102	Gaps 2;	4629 3992	4629	×800	4629	1220	<800

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REFERENCE
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslawkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Mihova, T., Minga, V., Murphy, T., Ragow, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stohbam, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., pollara,V., Raymond,C., Retta,R., Riaback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
Direct Submission
Direct Submission
Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On NOV 22, 2003 this sequence version replaced gi:38153914. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L26677
Center clone name: 409_K_22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR Web site: http://www-seq.wi.mit.edu
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56943
95967
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                                                                                                        gap of 100 bp
contig of 5593 bp in length
gap of 100 bp
contig of 5593 bp in length
contig of 2471 bp in length
gap of 100 bp
contig of 2471 bp in length
of 22340 bp in length
100 bp
of 22221 bp in length
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COMMENT

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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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Best Local S
Matches | 79
                              Query Match
Best Local :
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 856)

Paul, S.D., Linda, M.F., Rina, K., Douglas, K.R. and Laksmi, S.

Nucleic acid encoding sodium channel of nerve tissue
Patent: JP 1999235186-A 2 31-AUG-1999;

F HOFPMANN LA ROCHE AG

OS Homo sapiens (human)

N JP 199235186-A/2
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     l Similarity
74; Conserv
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C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12N15/02,C12P21/02,
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20-NOV-1998 JP 1998331769
20-NOV-1997 US 60/066225
PAUL SHATUA DAITORICHI,LINDA MARIE FISH,RINA KEIRU,
                                                                                                                                                                                                                                                                                                                               Key
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/clone_lib="RPCI-24 Male Mouse BAC"
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224271: contig of 14144 bp in length
224371: gap of 100 bp
241289: contig of 16918 bp in length.
                         13.5%;
88.1%;
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75.2%;
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Score 46.8; DB 6
Pred. No. 0.0031;
0; Mismatches
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Pred. No. 4.2e-05;
0; Mismatches 25
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AR340648
LOCUS
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ORGANISM
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BD217793
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                           46 TAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT
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AR340648
                                                                                                                                                                                                                                                                                                3701 Regulation of sodium channel BD217793
                                                                                                                                                                                   1 (bases 1 to 3701)
Hajj,S.D. and Waxman,S.
Regulation of sodium channel in posterior
Patent: JP 2002509860-A 3 02-APR-2002;
                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
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Nucleic acid encoding sodium channels in
Patent: US 6573067-A 6 03-JUN-2003;

Location/Qualifiers
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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                                                                                                                                                                                                                                                                                         BD217793.1
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                                                              C07K16/18,
C12N5/10, C12N15/09, C12P21/02, G01N33/566, G01N33/84, A61K37/02,
                                                                                            C07K14/435,A61K38/00,A61K39/395,A61K45/00,A61P25/04,A61P43/00,
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                                                                                                                                                                                                                                                                                         GI:33027563
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Pred. No. 0.0032;
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HSA417790
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-OCT-2001) Blum R., Institut fuer Physiologie, Submitted (25-OCT-2001) Blum R., Institut fuer Physiologie, Ludwig-Maximillians-Universitaet, Biedersteiner Strasse 29, 608, 80802 Muenchen, GERMANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         msA41/790 mRNA linear PRI 09-OCT-2002
Homo sapiens mRNA for voltage-gated sodium channel (NAV1.9 gene).
AIA17790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 419
22272672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Na (V) 1.9
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/db xref="SPTREMBL:Q8NDX3"
/translation="MDDRCYPVIFPDBRNEREPTSDSLAAIEKRIAIQKEKKKSKDQT
/translation="MDDRCYPVIFPDBRNEREPTSDSLAAIEKRIAIQKEKKKSKDQT
/translation="MDDRCYPVIFPDBRNEREPTSDSLAAIEKRIAIQKEKKKSKDQT
/ESUPQPRPQLDLXASRKLFKLYGDIPRELIGKPLEDTDFYRNHKTFMYLNKRRIYTR
FSAKHALFIFPGPNSIRSLAIRVSVHSLFSMFIGTVIINCVEMATGEAKNSNSNNTD
IABCVETGIYIFEALIKILARGFILDERSFLRDPWNWLDSIVIGIAIVSYIPGITIKL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                           /gene="NAV1.9"
/function="mediates neurotrophin-evoked neuronal
excitation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                    /product="voltage-gated sodium channel"
/protein_id="CAD10507.1"
/db_xref="GI:22796540"
                                                                                                                                                                                                /evidence=experimental
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                                                                                                                                                                                                                                         note="TTX-insensitive"
                                                                                                                                                                                                                                                                                                                                         gene="NAV1.9"
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                                                                                                                        xref="GOA:Q8NDX3"
                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                              type="neuroblastoma"
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Pred. No. 0.
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ORIGIN

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NLITLAVVTMAYEGOKKIVAAEIEAKEKMFORAQOLLKEEKERALVAMGIDRSSLTSLET
SYFTPEKERKLFGNKKKKSFFLRESGKIDQPGGDSDEDCQKKPQLLEQTKRLSQNLSLD
HFDEHGDLGQKRALSAVSLITITTMKEQSEKSQEECLE,CGERILASKYLTWNCCPQMLCV
KKVLRTVMTGPFTELAITICIIITMKEQSEKSQEECLE,CGERILASKYLTWNCCPQMLCV
KKVLRTVMTGPFTELAITICIIINTVELAMEHHKMEASFEKMINIGNLPFTSIFIAEM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADWMNCVLQKRSWPFLNSFRVLRVFTSIFIAEM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADWMNCVLQKRSWPFLRSFRVLRVFTSIFIAEM
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FTUNGFRAFCFFCC
SVDKKRPDQVEVAGGCAAQSKDIIFLVMEWKRGGSFTOEELGILTSVDKTLCMFDHF
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SVDKKRPDWVIWMLRKTCYQIVKHSWFESTIIFVLLSGALIFEDVHLENQFXIQE
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IYAAVDSTEKEQQPEFESNSLGYIFVVFIIFGSFTINLFJGVIIDMFNQQKXLGG
QDIEMTEEGKKYYNAMKKLGSKKPOKEIFRFLNKCQGLVPDIVTSQIFDIIISLIIL
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VLLSIVSTMLSTLENQEHIFPPTLFRIVALARIGRILRTLAFALRQYFFINGWLPDCVI
VLLSIVSTMLSTLENQEHIFPPTLFRIVALARIGRILRTLAFALRQYFFINGWLPDCVI
VLLSIVSTMLSTLENGEHIFPPTLFRIVALARIGRILRTLAFALRQYSTENGWNLFDCVV
VLLSIVSTMLSTLENGEHIFPSTATSTATOTATAVLAGALFERLAVAFNLKYQFL
PSLFNIGLLFIYATGTATAVLGGSDGLDSMKAMMEEKFMEANPLKKLYBPIVT
TTKRKEEERGAAIIQKAFRKYMMKVTKGDQGDQNDLENGPHSPLQTLCNGDLSSFGVA
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                                                                             Kanazawa, I., Goto, J. and Jeong, S.Y. Human sodium channel SCN12A and SCN8A Patent: WO 0190355-A 2 29-NOV-2001;
                                                                                                                                                                                                                                                                                                                     Homo sapiens
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WO 0190355-A/2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5728)
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                                                                                                                  ICHIRO KANAZAWA, JUN GOTO, SEON C12N15/12, C07K14/47, C07K16/18
                                                                                                                                                                       Homo sapiens (human)
WO 0190355-A/2
29-NOV-2001
                                                                                                                                             11-JUL-2000 WO 2000JP004629
23-MAY-2000 JP 00P 152085
                                                           Location/Qualifiers (200). (4534). Location/Qualifiers
         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0.0032;
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BD082952
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 5728)

CE Kanazawa,I., Goto,J. and Tei,Y.

Human sodium channel SCN12A
PAR SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)
PN JP 200137294-A/2
PD 27-NOV-2001
PP 23-MAY-2000 JP 2000152085
PI ICHIRO KANAZAWA,JUN GOTO, YOSHIHIRO TEI
PC C12N15/09,C07K14/47,C07K16/18/(C12P21/02,C12P21/08,C12N15/00
FT CDS

CC Location/Qualifiers

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                                                                                                                   Homo sapiens voltage-gated sodium channel alpha subunit, splice variant SCN12A-s (SCN12A) mRNA, complete cds. AF150882
AF150882.1 GI:6693704
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Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T.,
                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 5728)
                                                                             Homo sapiens
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0.0032;
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Ogata, K., Masuda, N.,
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Sequence 41 from patent
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Identification of a novel human voltage-gated sodium channel alpha
subunit gene, SCN12A
Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAY-1999) Neurology, Graduate Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tok
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Jeong, S.-Y., Suzuki,
                  AR340678
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Location/Qualifiers
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SWPTLNTLIKIIGNSVGALGNLTVVLVIVIFIFSVVGNQLFGRSFRNSQKSPKLCNPTG
PTVSCLRHWINGDFWHSFLVVFRILGEW IENWMECNQBANASSSLCVIVFILITVIG
KLVVLNLFIALLLNSFSNEERNGNLEGEARKTKVQLALDRFRRAFCFVRHTLEHFCHK
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVPFFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
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/codon_start=1
/product="voltage-gated sodium channel alpha subunit,
/protein id="AAF24980.1"
/db_xref="GI:6693705"
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GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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WLAFLAEBEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKPTSKOVGSVEIDMFSED
BYHLTIQDERKKSDVTSLISBCSTILDQDGFGWLPENVPKKQPERCLEKGFGCCFPC
SVDKRKPPWVIWMNLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVHLENQPKIQE
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HFDEHGDPLQRQRALSAVSILTIIMKEQEKSQEPCLPCGENLASKYLVWNCCPQWLCV
KKVLRTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT"
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                                                                                                                                                                                                                                                                       Score 46.8; DB 9
Pred. No. 0.0032;
0; Mismatches
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Unclassified.
Unclassified.
1 (bases 1 to 5860)
1 (bases 1 to 5860)
1 bb-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal root ganglia Nucleic Sideofo-A 41 03-JUN-2003;
Patent: US 6573067-A 41 03-JUN-2003;
Location/Qualifiers
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1. 5860
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Homo sapiens voltage-gated so
(SCN11A) mRNA, complete cds.
AF188679
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Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman,S.G.
Direct Submission
                                                                                                                                                                                                                                                                                                      Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A, Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA
                                                                                                                                                                                                                                                                                                                                                                                                               ganglion neurons
FEBS Lett. 462 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 6237)
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                /product="voltage-gated sodium channel type XI alpha
                                                      /gene="SCN11A"
/note="NaN alpha subunit; TTX-R sodium channel"
                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                           'gene="SCN11A"
                                                                                                                                                          tissue type="dorsal root ganglia"
. .6237
                                                                                                                                                                                                        db_xref="taxon:9606"
chromosome="3"
protein_id="AAF17480.1"
                                                                                                            gene="SCN11A"
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                            Kanazawa,I., Goto,J. and Jeong,S.Y.
Human sodium channel SCN12A and SCN8A
Patent: WO 0190355-A 1 29-NOV-2001,
JAPAN SCIENCE AND TECHNOLOGY CORP,ICHIRO KANAZAWA,JUN GOTO,
                                                                                                                                                                                                                                                                                                                                                                                                             Human sodium channel SCN12A
BD012082
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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KUVUNIJE IALLINS PSNEERNONLEGEARKTKVQLALDRFRRAFCFVRHTLEHFCHK
KUCKNJALPOOKEVAGGCAAOSKOI I PLYMEMKRGSETOEELGILTS VEKTLGVRHDWT
WLAPLAEEEDDVEFSGEDNAQRI TQPEPEQQAYELHQENKKOTSQRVOS VEELIDMFESD
BEHLTI ODPRKKSDVTS I LSECSTI DLODGFGWLPEMVEKKOPERCLEKGFGCCFPCC
SVDKRKPDWVLWMLRKTCYQI VKHSWFESFI I FVI ILLSSGALI FEDVHLENQPKI QE
LLNCTDI I FTHI FI LEMVLKWVAFGFGKYFTSAWCCLDF I I VI VSVTTLINIMELKSF
RTLRALRFLRALSQFEGMKVVVNALI GAI PAILNVLLVCLI FWLVFCI ILGVYFFSGKF
GKCINGTDS VLNYTI I TNKSQCESGNFSMI NOKVMFDNVGNATALLIQVAFFKGMMDI
I YAAVDSTEKEQOPEPENSISLGY I VFVVF I I FGSFFTILN TGVI IDNFNQOOKKLGG
QDI FWTESQKKYVNAMKKLGSKKPOKFI FRPLMKCQGLVFDI VTSQI FDI I I 151 I IL
NNI SMYABES YNOPKAMKSI LDHLINWFVVI FTLECLIK IF FALRVYFTINGWNLI FDLVV

MISMYABES YNOPKAMKSI LDHLINWFVVI FTLECLIK IF FALRVYFTINGWNLI FDLVV
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VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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PSLFNIGLLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSMLCLFQISTSAG
WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
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GEVPQPRPQLDLKASRKLPKLYGDIFRELIGKPLEDLDPFYRNHKTFMYLNRKRTIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNUNNTD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 6528)

CE 1 (bases 1 to 6528)

RS Kanazawa,I., Goto,J. and Tei,Y.

Human sodium channel SCN12A

Patent: JP 200137794-A 1 27-NOV-2001;

APAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001377294-A/1

PD 27-NOV-2000

PP 23-MAY-2000 JP 2000152085

PI ICHIRO KANAZAWA,JUN GOTO, YOSHIHIRO TEI

PC C12N15/09, C07K14/47, C07K16/18/C12P21/02, C12P21/08, C12N15/00

CC

FH Key Location/Qualifiers

FT CDS Location/Qualifiers
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1 Similarity 88.1%;
74; Conservative
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23-MAY-2000 JP 00P 152085
ICHIRO KANAZAWA,JUN GOTO,SEON YONG JEONG
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WO 0190355-A/1
29-NOV-2001
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Location/Qualifiers
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Search completed: March 22, 2004, 19:32:29 Job time : 1846.35 secs

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## ALIGNMENTS

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RESULT 1
                                   AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a
                                                                                                                                                                                                                                                                                                                                                                  Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
 Sequence 346 BP; 101 A; 71 C;
                                                                                                                                                                                          Grose
                                                                                                                                                                                                                                                                                                                     WO9947670-A1
                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                              Claim 6; Page 67; 73pp; English.
                                                                                                                                      Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                WPI; 1999-562112/47.
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                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
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                          for the treatment of pain or hypersensitivity
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Query Match
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Conservative

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                                                                                    The present sequence encodes a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy; neuropathic pain; migraine; headache; ss.
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   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and especially neuropathic pain, e.g. migraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fish LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0066225P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98FR-00014551
   251 A; 172 C; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA; 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sodium channel protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabert
   G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    얁
                                                                                                                                                                                                                                                                                                                                                                                    the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sangameswaran L;
                                                                                                                                                                                                                                                                                                                                                                                 system
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                                                                 and headache
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Query Match Best Local Similarity

13.5**%**; 88.1**%**;

Score Pred.

46.8; DB 2; No. 5.4e-05;

Length 856;

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46

TAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT

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                                                                                         This is the nucleotide sequence of a partial cDNA clone which codes for a comparison (see AAY06596) of human NaN, a previously unidentified voltage cc gated sodium channel protein that is preferentially expressed in dorsal croot ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R cc sodium current. The NaN channel cDNA was obtained from human DRG tissue cDNA by PCR amplification (see also AAX87620-22). Rat, mouse and human cc NaN nucleic acids (see AAX8760-02) and polypeptides (see AAX06596-98) cc are provided. The invention also includes expression vectors and cc transformed host cells, methods for identifying tissues and cells that cc express NaN, methods for identifying agents that modulate NaN channel cc express NaN, methods for identifying agents that modulate NaN channel cc express NaN, methods for identifying agents that modulate nan amethod for using such agents to treat acute or chronic pain, paraesthesia and cc hyperexcitability phenomena. The preferential expression of NaN in cc sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other crowd cells in the brain and spinal cord. The gene is named SCN11a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NaN; sodium channel; ion transport; human; dorsal root ganglia; pain; paraesthėsia; hyperexcitability; therapy; SCN11a gene; ss.
                                                                Sequence 3638 BP;
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 8A1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human sodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX87602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX87602 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                   phenomena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYYA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
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                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAACTTAATGGAATTGAAGTCCTTCCGGACTCTACGAGCACTGAGGCCTCTTCGTGCGCT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCCAGTTTGAAGGAATGAAGGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCCAGTTTGAAGGAATGAAGGT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids encoding sodium channels, used to develop treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel
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98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US002008
                                                                1027 A; 793
                                                                                                                                                                                                                                                                                                                                                                    91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                  13.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
   Score 46.8; DB
Pred. No. 0.0001
0; Mismatches
                                                                C; 801 G; 1016 T; 0 U; 1 Other;
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J.0001;
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                                                                                                 The present sequence is that of a partial cDNA for a novel human content of the trodotoxin resistant sodium channel, termed NaN (see AAB20125). The content of the content 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraeqthesia and/or hyperexcitability phenomena.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Fig 8A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB20125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200105831-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperexcitability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sodium channel NaN partial cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2754 TAACTTAATGGAATTGAAGTCCTTCCGGACTCTACGAGCACTGAGGCCTCTTCGTGCGCT 2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-103147/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 3701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCCAGTTTGAAGGAATGAAGGT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waxman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
    BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00354147
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1. .3699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; human; tetrodotoxin resistant; pain; paraesthesia;
analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
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Query Match Best Local Similarity

13.5%;

Pred. No. 0.0001;

DB 4;

Length 3701;

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TAACTTRATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT

Matches Query Match Best Local (

Similarity

13.5%;

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Score 46.8; DB 6; Pred. No. 0.00012; 0; Mismatches 7;

Length 5728;

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Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T;

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RESULT 5
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                                                                    subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A-s sodium channel
                                                                                                                                                                                                                                                                                                                                                                         Sodium channel alpha subunits SCN12A and SCN8A of human nervous s together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; human nervous system; chromosome 3p23-21.3; excitatory cell; drug development; familial hyperglycaemia; OT extending syndrome type
                                                                                                                                                                                                The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel
                                                                                                                                                                                                                                                                                                                               Claim 7; Page 55-70; 118pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanazawa I, Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2000; 2000JP-00152085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human sodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL42750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL42750 standard;
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200. .4534
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                                                                                                                                                                            The present sequence is that of cDNA encoding a novel human tetrodotoxin cresistant sodium channel, termed NaN (see ABE0121). The cDNA was considered from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also ABF20122-2). NaN belongs to the a-subunit courrent. Such channels underlie the generation and propagation of current. Such channels underlie the generation and propagation of cimpulses in excitable cells such as neurons and muscle fibres.

CC preferential expression of NaN on sensory neurons innervating the body concerns, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed comethod of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates tringeninal neurons. NaN nucleic acids are used in gene therapy to correct disorders associated with decreased sodium channel expression or candinatense to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN polypeptides
      Matches
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                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 11A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB20121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dib-Hajj S, Waxman SG
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                   The present invention describes an expression vector comprising a nucleic card sequence that encodes a mammalian Na v 1.9 sodium channel protein or cits fragment, and producing a sodium current when transfected in a cell. Riso described: (1) a recombinant cell comprising the plasmid selected comprising the plasmid selected comprising the plasmid selected comprising the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 codium channel-dependent sodium current by: (a) providing a cell that has seen transfected with the expression vector; and (b) culturing the cell cunder conditions that allow expression of Na v 1.9 sodium channel protein compression that allow expression of Na v 1.9 sodium channel protein compression to produce a sodium current into the transfected cell; (3) a method of composing the cell or cell line produced by the method to the agent; and (c) exposing the cell or cell line produced by the method to the agent; and comprising the expression vector. The agent, where an cell acceptable of modulating sodium current is indicative of an agent comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel at currents in dorsal root ganglion neurons. The comprising compression of the Na v 1.9 sodium channel at currents are useful channel sequence encodes a human Na v 1.9 sodium channel protein, which compression the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acsequence that encodes a mammalian Nav1.9 sodium channel protein or it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2003.
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/product= "Na v 1.9 sodium channel protein"
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                                                                                                                                                          The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A sodium channel subunit
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanazawa I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAY-2000; 2000JP-00152085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-393394/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                6; Page 29-46; 118pp; Japanese.
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     74;
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                                                                                                        6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCCAGTTTGAAGGAATGAAGGT 3527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA; 6528
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        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel subunit SCN12A coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '*tag=
                        13.5%;
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Score 46.8; DB 6;
Pred. No. 0.00013;
0; Mismatches 7
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Pred. No. 0.00013;
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                                                       DB 6;
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22-AUG-2000;

22-AUG-2000;

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23-AUG-2000;

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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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18-AUG-2000;
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14-AUG-2000;
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26-JUL-2000;
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11-JUL-2000;
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19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic
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                                                                                                                                             14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune/haematopoietic antigen
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2000US-0179065P

2000US-0184664P

2000US-0184664P

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2000US-0184664P

2000US-0199076P

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2000US-0225758P

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2000US-0225734P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic sequence
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06-SEP-2000; 06-SEP-2000; 08-SEP-2000;

2000US-0230437P. 2000US-0230438P. 2000US-0231242P.

08-SEP-2000 08-SEP-2000 12-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000

2000US-0231968P. 2000US-0232397P. 2000US-0232398P. 2000US-0232080P

2000US-0232399P 2000US-0232400P 2000US-0232401P 2000US-0233063P

2000US-0233064P.
2000US-0234065P.
2000US-0234274P.
2000US-0234274P.
2000US-0234997P.
2000US-0235484P.
2000US-0235834P.
2000US-0235834P.

2000US-0236327P. 2000US-0236367P. 2000US-0236368P.

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RESULT 10
AAK82628/c
ID AAK82628 standard; DNA; 48203 BP.
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                                                                                                                                                                                                                                                                                                                                                                                               CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) cyroteins and polynucleotides may be used in the prevention, diagnostis and creatment of diseases associated with inappropriate (I) expression. For creatment of diseases associated with inappropriate (I) expression. For creatment of diseases associated with inappropriate (I) expression. For creatment of diseases associated with inappropriate (I) expression. For creatment in the prevention, diagnosis and creatment the patients of the deletions or deletions in a patient's genome created that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) created a host cell and culturing the cell to express the created (I) proteins and polynucleotides may be used to prevent, (I) proteins and polynucleotides may be used to prevent, (I) created and cancer metastases of haematopoietic diseases, especially concers and cancer metastases of haematopoietic derived cells. AAK64703 created to a prevent the present human immune/haematopoietic antigen genomic created represent invention. AAK54942 to AAK54950 and AAM82169 creates.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 69
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17-NOV-2000;
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06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 13578 BP; 3665 A; 2559 C; 2623 G; 4731 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 36474; 3071pp + Sequence Listing; English.
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Similarity 55.6%;
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2000US-025193P.

2000US-0251858P.

2000US-0251869P.

2000US-0251969P.

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                                                                                                                                                                                                                                                                                                                 Score 36; DB 4; Length 13578; Pred. No. 0.76;
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2000US-0239935P.
2000US-0239935P.
2000US-0241786P.
2000US-0241786P.

14-SEP-2000
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21-SEP-2000
21-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
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29-SEP-2000
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2000US-0246528P.
2000US-0246528P.
2000US-024651P.
2000US-024921P.

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Best Local 9
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   WO200157182-A2
                              Homo sapiens.
                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36475
                                                                                                                                 07-NOV-2001
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                                                    GENOME
                                                       SCI INC
Ruben SM
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000;

; 2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P. ; 2000US-0189874P. 2000US-0199873P. ; 2000US-0198133P. ; 2000US-0205515P.

09-AUG-2001.

WO200157182-A2 Homo sapiens. cytostatic; gene

17-JAN-2001; 2001WO-US001354.

Human; immune; haematopoietic;

therapy; vaccine;

metastasis;

06-NOV-2001 (first entry)

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24973.

immune/haematopoietic antigen; cancer;

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RESULT 12
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XX DE Human :
XX Human :
XX Human;
XX Cytost.
XX Cytost.
XX Homo s:
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07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 07-JUL-2000; 11-JUL-2000; 11-JUL-2000;

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20-NOV-2000;
01-NOV-2000;
08-NOV-2000;
09-DC-2000;
                                                                                                                      Nucleic
useful f
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I amino acid sequences given in AAM82170 to AAM91921. (I) have cytostati activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                            Disclosure;
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                                                                                                                                                                                                                SCI
                                                                                            24973; 3071pp +
                                                                                                                   human immune/hematopoietic diagnosing and/or treating
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                                                                                            Sequence Listing;
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antigen

polypeptides, and metastasis.

English.

c antigen (I) ve cytostatic uction. (I)

and

2000US-0209467P.
2000US-0215135P.
2000US-021647P.
2000US-021647P.
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14-JUL-2000 26-JUL-2000 26-JUL-2000 14-AUG-2000 16-SEP-2000 17-SEP-2000 18-SEP-2000 19-SEP-2000 11-SEP-2000 11-SE

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RESULT 13
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XX Human
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Matches 69
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04-FEB 2000

24-FEB 2000

02-MAR 2000

16-MAR 2000

17-MAR 2000

19-MAY 2000

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07-JUN 2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune/haematopoietic antigen genomic sequence SEQ ID NO:36478.
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atic; gene therapy; vaccine; metastasis; ds.
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3-0250391P.
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(HUMA-) HUMAN GENOME SCI INC

Ç, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 36478; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the CC nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic to AAK67694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK34942 to AAK64903 and AAM82169 corresponded to the present incoming the production of the control of the represent sequences used in the exemplification of the present invention

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Sequence 48204 BP; 13147 A; 9074 C; 10292 G; 15691 T;
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U; 0 Other;
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RESULT 14

RAKES 630/0

ID AAK88

XX AAK88

AC AAK88

XX DT 07-NC

XX CTCS

XX Human

XX Human

XX Homo

OS Homo

XX Homo

XX Homo

XX Homo

PN 09-AI

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Best Local S
Matches 69
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK82630 standard; DNA; 48204 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001; 2001WO-US001354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAATTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAACTAGAATATTAAGAGACTGCTGGCAAGGCAAGCAGTTAATTTTCAGTTGAAATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTT 17203
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2000US-0225758P.
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2000US-0226868P.
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Pred. No. 1.3;
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2000US-0232081P.
2000US-023239FP.
2000US-023239FP.
2000US-023239FP.

2000US-0232400P. 2000US-0232401P.

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                                                                                                                                                                                                                 amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cytostations and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to cuplement the patients own production of (I). Additionally, (I) colored and the patients own production of (I). Additionally, (I) colored acids into a host cell and culturing the cell to express the crotein. (I) proteins and polynucleotides may be used to prevent, conserved and cancer metastases of haematopoietic decides, especially connects and cancer metastases of haematopoietic decides and AAK64703 connects from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                          Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2000;
01-DEC-2000;
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11-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                         Sequence 48204 BP; 15691 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 37442; 3071pp + Sequence Listing; English.
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31065 ATTAAATAGAAAGTATTTTCTTGCTTTGTGGAAGCACGTGAATTTTTTAAAAAAGCTGCT 31006
                                                                                               148
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                              208 CTTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAATTTGAG 267
                                                                                                                             69;
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                                                                                                                                              Similarity
                                                                                AGAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTC
                                                               AGAACTAGAATATTAAGAGACTGCTGGCAAGGCAAGCAGTTAATTTTCAGTTGAAATTGC
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2000US-0249297P.
2000US-0249297P.
2000US-025963P.
2000US-025963P.
2000US-0251869P.
                                                                                                                           Conservative
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                                                                                                                                         10.4%;
55.6%;
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                                                                                                                           Score 36; DB 4
Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                       10292 C; 9074 G;
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                                                                                                                             Gaps
                                                                 31066
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RESULT 15
AAK70164/c
ID AAK70164;

XC AAK70164;

XX AAK70164;

XX AAK70164;

XX DAK70164;

XX DE Human immune/haematopoietic antigen XX DAK70182-A2.

XX D9-AUG-2001.

XX D9-AUG-
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08-SEP-2000

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12-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                  CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC supplement the patients own production of (I). Additionally, (I) croteins (I) proteins and polynucleotides may be used to proceed the secreted (I), by inserting the CC protein. (I) proteins and polynucleotides may be used to prevent, (CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic actived cells. AAK64703 cc AAK87694 represent human immune/haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                         Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                    Sequençe 48204 BP; 15691 A; 10292 C; 9074 G; 13147 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                     148 AGAAGTTCAGTTAACAGAGAAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTC 207
                                                                                                                                                                                        208 CTTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAATTTGAG 267
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2000US-0254097P.
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6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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-6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
-6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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US-10-27-632-97040
US-10-027-632-97041
US-10-027-632-319123
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US-10-067-514-1
US-10-419-723-1
US-10-388-470-4
US-10-388-470-1
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Sequence 41, Appl
Sequence 97040, A
Sequence 97041, A
Sequence 319122,
Sequence 319123,
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Sequence 1, Appli
Sequence 27, Appli
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## ALIGNMENTS

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RESULT 1

US-10-388-470-6

US-10-388-470-6

Sequence 6, Application US/10388470

Publication No. US20030228662A1

GENERAL INFORMATION:

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Maxman, Stephen 6,

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT PILING DATE: 1903-01-19

PRIOR APPLICATION NUMBER: US/09/354,147C

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US/09/354,147C

PRIOR APPLICATION NUMBER: US/09/09/402

PRIOR APPLICATION NUMBER: US/09/09/402

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: US/09/02008

PRIOR FILING DATE: 1999-01-29

NUMBER: PATURE: 1999-01-29

NUMBER: PATURE: PATURE: PATURE: PATURE: UNA
ORGANISM: Homo sapiens

PRATURE: NAMB/KEY: Unsure
LOCATION: (21). (3699)

OTHER INFORMATION: Partial human NAN CDNA sequence

PRATURE: UNSURE UNSURE US/09/402

PRIOR APPLICATION: PARTIAL human NAN CDNA sequence

PRATURE: UNSURE US/09/402

OTHER INFORMATION: PARTIAL human NAN CDNA sequence

PRATURE: UNSURE US/09/402

OTHER INFORMATION: PARTIAL human NAN CDNA sequence

PRATURE: UNSURE US/09/402

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; Sequence 41, Application US/10388470
; Publication No. US20030228662A1
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                                                                                                                                                                                                                                                                                                         Sequence 97040, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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SEQ ID NO 41
LENGTH: 5860
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                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
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APPLICANT: Waxman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE:
NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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les 74; Conserv
                                              APPLICATION NUMBER: US 60/193,483
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APPLICATION NUMBER: US 60/185,218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 TAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT 102
                        LING DATE: 2000-03-29
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Pred. No. 0.00011;
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US-10-027-632-97041/c
; Sequence 97041, Application US/10027632
; Publication No. US20030204075A9
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; ORGANISM: Human
US-10-027-632-97040
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; ORGANISM: Human
US-10-027-632-97041
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 97041
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR ALPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 667
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                           381 ATCAATAGTTAAGAATGCCCTGGGTAAGTTATTTGCCTGMCTA 339
                                                                       209 TTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAGCCTGCCCA 251
                                                                                                                        441 GATATGCTTTGCACAATGCAAGTTGCAAATGCCAAAGTTCATTCTTCYGCTGTAATATTC
                                                                                                                                                                  149 GAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTCC
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                                                                                                                                                                                                              Score 37; DB 15; I pred. No. 0.081; 1; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Version 4.0
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Pred. No. 0.081;
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/167,363
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; ORGANISM: Human
US-10-027-632-319122
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 319123, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 319122
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Publication No. US20030204075A9
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 0560/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
                         PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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APPLICATION NUMBER: US 60/146,002
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SEQ ID NOS: 325720
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Pred. No. 0.081;
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Publication No. US/20040014099A1
GENERAL INFORMATION:
APPLICANT: Gretarsdottir, Solveig
APPLICANT: Jonsdottir, Sif
APPLICANT: Reynisdottir, Sigridur Ti
APPLICANT: Thorleifsson, Gudmar
APPLICANT: Gulcher, Jeffrey
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APPLICANT: Gulcher, Jeffrey
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
FILE REFERENCE: 2345.2010-005
CURRENT APPLICATION NUMBER: US/10/419,723
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: 10/255,120
PRIOR APPLICATION NUMBER: 10/067,514

Reynisdottir, Sigridur Th. Thorleifsson, Gudmar

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US-10-067-514-1/c
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; ORGANISM: Human
US-10-027-632-319123
US-10-419-723-1/c
                                                                                                                                                                                                                                                                                                US-10-067-514-1
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APPLICANT: Gretarsdottir, Solveig
APPLICANT: Jonedottir, Sif
APPLICANT: Reynisdottir, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
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                                                                                                                                                                                                                     Matches 60;
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO
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Publication No. US20030054531A1
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CURRENT APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-02-04
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/811/352
                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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                                                                      809976 TCTCTCCTATTTTTGAAGTTTAGAGGAAGAAACTGCCT 809937
                                                                                                                                                 810036 CÁGCTCAGATGAGGCTCACTTTTGCTGAACTTCAGATGCTTTTATCATTTTTCCTTACAAT 809977
                                                                                                          244 CCTGCCCAGTGCTTAGAATTTGAGGGGTAGAGAAAAGCCT 283
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                                                                                                                                                                                                                                        h 10.4%;
Similarity 60.0%;
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Pred. No. 0.081;
1; Mismatches
                                                                                                                                                                                                                     Score 36; DB Pred. No. 8.3; 0; Mismatches
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; NAME/KEY: unsure
; LOCATION: (5804)
; OTHER INFORMATION: cDNA sequence of mouse NaN, n
US-10-388-470-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 09/811,352
PRIOR FILING DATE: 2001-03-19
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
CURRENT FILING DATE: 2003-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 44
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APPLICANT: Waxman,
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (19)..(5313)
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5822
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3446
                                                                            3386 AGTCCTTCCGGAATCTGCGAGCCCTGAGACCTCTGCGGGCACTGTCTCAGTTTGAAGGAA 3445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 CAGTTCTTTTTGGGCTGAGAFTTCCTTAAATTGCCAAGCTTTTCCTGGGTTACTTACCAG
                                       120 TGAAGGT 126
                                                                                                          61 AGAACCTTCCGGATCTACGAGCACTGAGGCCTCT-CGTGCGCTGTCCCAGTTTGAAGGAA 119
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TGAAGGT 3452
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                                                                                                                                                                            10.3%;
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Pred. No. 0.6;
0; Mismatches
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Pred. No. 8.3;
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US-10-388-470-1

RESULT 10

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US-10-260-877-27/c
; Sequence 27, Application US/10260877
; Publication No. US20030021813A1
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                                                                                                                 APPLICANT: Chovan, Linda E.
APPLICANT: Chovan, Linda E.
APPLICANT: Hessler, Paul E.
APPLICANT: Reich, Karl A.
TITLE OF INVENTION: ESSENTIAL BACTERIA GENES ANI
TITLE OF INVENTION: SCANNING IN HAEMOPHILUS IN.
TITLE OF INVENTION: 'ESSENTIAL GENES'
FILE REFERENCE: 6565.US.Pl
CURRENT APPLICATION NUMBER: US/10/260,877
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/649,145
PRIOR APPLICATION NUMBER: US/09/649,145
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR PFLING DATE: 1999-07-16
PRIOR PFLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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                                                                                                    SEQ ID NO 27
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Best Local
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APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: (1996)..(4042) CITHER INFORMATION: n = a or c or g or t. Xaa at amino acid position OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn OTHER INFORMATION: or Lys.
LENGTH: 2364
TYPE: DNA
ORGANISM: H. influenzae
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: cDNA sequence for rat NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5875
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
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Pred. No. 0.
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; OTHER INFORMATION: HI-0061
US-10-260-877-27
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEOFING Sequence of the Haemophilus
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-04-21
PRIOR PILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fleischmann et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (4747)...(4747)
OTHER_INFORMATION: n equals
              NAME/KEÝ: misc feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals
                                                                                                       NAME/KEY: misc feature
LOCATION: (36551)..(36551)
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LOCATION: (36543) ...(36543)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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                                                                                      OTHER INFORMATION: n equals
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LOCATION: (9921)..(992
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OCATION: (10150)..(10150)
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Pred. No. 0.84;
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NAME/KEY: misc feature
LOCATION: (45593)..(45593)
                               NAME/KEY: misc_feature
LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
                                                                                                     NAME/KEY: misc feature
LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (65313)...(65313)
OTHER INFORMATION: n equals
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals
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LOCATION: (51602)...(51602)
OTHER INFORMATION: n equal
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LOCATION: (47036)..(47036)
OTHER_INFORMATION: n equals
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LOCATION: (44905)...(44905)
OTHER INFORMATION: n equals
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equal
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LOCATION: (44975)..(44975)
NAME/KEY: misc_feature
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NAME/KEY: misc\_feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equals equals a a 'n a þ ļ ŗ רָ ļ 'n ω ω Q g õ မ္ မ္က 얁 õ

NAME/KEY: misc feature LOCATION: (45732)..(45732) OTHER INFORMATION: n equals OTHER INFORMATION: n equals ā ŗ Q or

NAME/KEY: misc feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals a a ğ ŗ g õ õ

NAME/KEY: misc feature LOCATION: (51786)..(51786) OTHER INFORMATION: n equals equals ā a Ĺ ļ မ္ပ 유

NAME/KEY: misc feature LOCATION: (55369)..(55369) OTHER INFORMATION: n equals a a ŗ Ĺ ω ç ç

NAME/KEY: misc\_feature LOCATION: (65309)..(65309) OTHER\_INFORMATION: n equals ā , g õ

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NAME/KEY: misc\_feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a Ĺ ω õ

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NAME/KEY: misc feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a,
FEATURE:
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OTHER INFORMATION: n equals
                                   NAME/KEY: misc_feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
                                                                                 NAME/KEY: misc_feature
LOCATION: (147197)..(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942) ... (145942)
OTHER INFORMATION: n equals
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER_INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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TOCATION: (142750)..(142750)
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LOCATION: (131360)..(131360)
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US-10-329-670-1
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LENGTH: 18
TYPE: DNA
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Best Local
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PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/329,670 CURRENT FILING DATE: 2002-12-24 PRIOR APPLICATION NUMBER: US 09/643,990
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TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragn
TITLE OF INVENTION: Thereof, and Uses Thereof
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                                                                                                                       NAME/KEY: misc_feature
LOCATION: (36543)..(36543)
OTHER_INFORMATION: n equal
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals
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LOCATION: (10150)...(10150)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (9921)..(992
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NAME/KEY: misc_feature
LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,
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PEATURE: NAME/KEY: misc_feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (44975)...(44975)
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LOCATION: (44905)..(44905)
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LOCATION: (44416)...(44416)
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals
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LOCATION: (80024)...(80024)
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LOCATION: (65313)...(65313)
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LOCATION: (51786)..(51786)
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LOCATION: (51602)..(51602)
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LOCATION: (47036)..(47036)
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LOCATION: (142750)..(142750)
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LOCATION: (140398)..(140398)
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LOCATION: (122336)..(122336)
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OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
                        FEATURE:

NAME/KEY: misc feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
                                                                                                                        NAME/KEY: misc feature
LOCATION: (145942)...(145942)
OTHER INFORMATION: n equals
                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (145171)...(145171)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER_INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (131340)..(131340)
OTHER_INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (121344) ... (121344)
OTHER INFORMATION: n equals
                                                                         OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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LOCATION: (147197)..(147197)
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Best Local S
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Publication No. US20020173635A1
GENERAL INFORMATION:
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Query Match
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LOCATION: (152530)..(152530)
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OTHER INFORMATION: n equals
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                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 666:
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MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/040,739

PILING DATE: 07-Jan-2002

CLASSIFICATION: <UNLOWNDER:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
                                                                                                                                                                                                                                  NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                       SEQUENCE DESCRIPTION:
                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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1 Similarity 54.8%;
69; Conservation
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                                                                                                                                                                                                 TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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                                                                                                        STRANDEDNESS: double
                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                    TELEPHONE:
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McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                    (617)
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                                                   SEQ ID NO: 666:
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Score 34.2;
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DB 13;
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Length 444;
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RESULT 15
US-10-029-386-5767/c
Sequence 5767, Application US/10029386
Publication US: 10029386
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Search completed: March 23, Job time: 303.915 secs
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SEQ ID NO 5767
LENGTH: 525
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE |
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC009086.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: NT HIT: 9114775898, EVALUE 1.700+101
OTHER INFORMATION: SWISSPROT HIT: P07954, EVALUE 1.700+00
OTHER INFORMATION: EST_HUMAN HIT: BF819829.1, EVALUE 0.000+00
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0; Mismatches
                                                                                                                                                                                                                                                                                     Score 34.2; DB 14;
Pred. No. 0.64;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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Perfect score:
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US-09-646-224A-12

Sequence 12, Application US/09646224A

GENERAL INFORMATION:

APPLICANT: Glaxo Wellcome PLC
APPLICANT: Tate, Simon N

APPLICANT: Hicks, Caroline A

TITLE OF INVENTION: Ion Channels

FILE REFERENCE: PG3432

CURRENT APPLICATION NUMBER: US/09/646,224A

CURRENT APPLICATION NUMBER: GB 9805793.8

PRIOR APPLICATION NUMBER: GB 9805793.8

PRIOR APPLICATION NUMBER: US/09-646,224A

CURRENT FILING DATE: 1998-03-18

SOFTWARE: PRIOR DATE: 1988-03-18

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 346

TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
FEATURE
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84151
; LENGTH: 115159
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Best Local Similarity
Matches 346; Conserv
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282; Conservat
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TTTTCCTGGGTTACTTACCAGCCTGCCCAGTGCTTAGAATTTGAGGGGTAGAGAAAAGCC
                                                                                                                                                                      AGAGAAAGGTGGAAAGACCAACAGTTCTTTTTGGGCTGAGATTTCCTTTAAATTGCCAAGC
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100.0%; Pred. No. 5.5e-97;
tive 0; Mismatches 0;
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Pred. No. 6.9e-68;
2; Mismatches 7;
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: LENGTH: 6925
: TYPE: DNA
: ORGANISM: HUMAN
US-60-207-214-72
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPOR
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000581
CURRENT APPLICATION NUMBER: US/60/207,214
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 622
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                  US-60-466-412-152344;
; Sequence 152344, Application US/60466412
; GENERAL INFORMATION:
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                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-466-412-152344
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                                                                                                                                                            FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 152344
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Best Local Similarity 96.3
Matches 283; Conservative
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Sequence 72, Application US/60207214
GENERAL INFORMATION:
Query Match
Best Local Similarity 99.
Matches 197; Conservative
                                                                                                                                                                                                                                                                              APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                           LENGTH:
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                  57.1%;
99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.8%;
Score 197.6; DB 1
Pred. No. 1.1e-50;
1; Mismatches (
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Pred. No. 4.2e-68;
0; Mismatches 8;
                                     DB 103;
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                                        SEQ ID NO 3
LENGTH: 856
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
                                                                                                    FILE REFERENCE: R0021B-REG
CURRENT APPLICATION NUMBER: US/09/195,851
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 60/066,225
EARLIER FILING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                         APPLICANT: Fish, Linda M.
APPLICANT: Khare, Reena
APPLICANT: Rabert, Douglas K.
APPLICANT: Sangameswaran, Lakshmi
TITLE OF INVENTION: A Voltage-Gated Nervous Tissue Sodium Channel,
TITLE OF INVENTION: Polynucleotides Encoding Therefor, and Methods of Use
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2003-04-30 NUMBER OF SEQ ID NOS: 429241
                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dietrich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 AGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGAAAAGACCAACAGTTCTTTTTGGGC
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Pred. No. 2.1e-21;
1; Mismatches 1;
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Query Match
Best Local Similarity
Thes 74; Conserva
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US-60-213-846-1412
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PCT-US00-19342-6
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
                                                                                                                                                                                                                                                                                                                Sequence 6, Application PC/TUS0019342
GENERAL INFORMATION:
APPLICANT: Vale University
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1412
LENGTH: 3163
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                                                                                                                                                                        SOFTWARE:
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ORGANISM: HUMAN
-60-213-846-1412
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US00/19342
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/354,147
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                        NAME/KEY: CDS
LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN
                                                                                                                     TYPE: DNA
ORGANISM: Homo
                  NAME/KEY: unsure LOCATION: (922)
                                                                                                          FEATURE:
                                                                                                                                                          LENGTH:
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INFORMATION:
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                                                                                                                                                                                           PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                    Modulation of Sodium Channels in
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Pred. No. 0.0045;
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Pred. No. 0.
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                                                   cDNA sequence
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0.0027;
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              APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in
FILE REFERENCE: 44574-5004-01-US
FULRENT APPLICATION NUMBER: US/10/388,470
CURRENT APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
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NAME/KEY: unsure
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OTHER INFORMATION: y =
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OTHER INFORMATION: partial human NaN
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NAME/KEY: CDS
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 APPLICATION NUMBER:
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Pred. No. 0.0048;
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Length 3701;

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Dorsal

Root Ganglia

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APPLICANT: Yale University
TITLE OF INVENTION: Dorsal Root Ganglia-Specific and Tet
TITLE OF INVENTION: Dorsal Root Ganglia-Specific and Tet
TITLE OF INVENTION: Oblage-Gated Sodium Channel, S. Dib
FILE REFERENCE: 44574-5004-WO, Yale University
CURRENT APPLICATION NUMBER: PCT/US99/02008D
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 60/072,990
EARLIER APPLICATION NUMBER: US 60/072,990
EARLIER APPLICATION NUMBER: US 60/109,402
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 40
NUMBER OF SEQ ID NOS: 40
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Pred. No. 0.0048;
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Dib-Hajj et al.
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US-60-453.050-2171, Application US/60453050

Sequence 2171, Application US/60453050

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, MAY
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
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US-10-170-235-13985
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US-10-170-235-13985
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Matches
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CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 13985
LENGTH: 5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13985, Application US/10170235

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
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LOCATION: (922)
OTHER INFORMATION: y = c
OTHER INFORMATION: Leu.
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LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
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ORGANISM: Homo sapiens
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Similarity 88.1%;
74; Conservative
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Pred. No. 0.0054;
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Pred. No. 0.0048;
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Sequence 2171, Application US/60466412

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: LAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT APPLICATION NUMBER : US/60/466,412
CURRENT APPLICATION STATE CONSTRUCTION OF SEQ ID NOS: 429241
SOFTMARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
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US-60-453-135-2171
; Sequence 2171, Application US/60453135
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-60-453-135-2171
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; ORGANISM: Homo sapiens
US-60-466-412-2171
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
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NUMBER OF SEQ ID NOS: 82762
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2171
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APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DEF
FILE REFERENCE: CL001456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
                                       TYPE: DNA
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Similarity 88.1%;
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88.1%;
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US-10-219-051B-910

(Sequence 910, Application US/10219051B

(GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain
FILE REFERENCE: LeA 35633 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 14715
SOFTWARE: Perl script
SOFTWARE: Perl script
SOFTWARE: Perl script
TYPE: DNA
ORGANISM: Homo sapiens
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Search completed: March 23, 2004, 04:00:14
Job time : 2619.4 secs
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Best Local Similarity 88.1%;
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)..(5728)
OTHER INFORMATION: n=a, c, g or t
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: EMBL / AF150882
DATABASE ENTRY DATE: 2000-01-16
                                                                                                                                                                                                                                  3613 TAACTTAATGGAATTGAAGTCCTTCCGGACTCTACGAGCACTGAGGCCTCTTCGTGCGCT 3672
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                                                                                                                  GTCCCAGTTTGAAGGAATGAAGGT 3696
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                10.1 659
9.8 62555
9.5 304123
9.0 304123
9.0 14900
8.9 11647
8.9 21872
8.8 1126118
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Copyright (c) 1993 - 2004 Compugen Ltd.
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  Sequence 208, App Sequence 1073, Ap Sequence 1073, Ap Sequence 12785, A Sequence 12785, A Sequence 12785, A Sequence 12479, A Sequence 12479, A Sequence 12499, A Sequence 12430, A Sequence 21000, A Sequence 21000, A Sequence 21006, A Sequence 21089, A Sequence 21089, A Sequence 21089, A Sequence 21706, A Sequence 10552, App Sequence 10552, App Sequence 10563, A Sequence
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319 GCC    42 ACC	259 GAZ   102 AAC	199 TGF 	Match Local Simi es 72;	ORGANISM: Homo sap FEATURE: NAME/KEY: variatio LOCATION: 6, 648 OTHER INFORMATION: 0-474-495-208	208 659 A	APPLICA FILING R OF SEQ ARE: Pat	E PE	REF		495-20 208,		2 8 8	28	221	) 22 K	യയ		ω.	28.6 28.4		8
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GCCAAGATGAGCTG             ACCACGATGCACTG	AGGGGTA	TCCTTAA        AACCTAA	10 53 vativ	n is		108: 264 108: 264		ERENCE: 1422-0606P APPLICATION NUMBER:	: WA, Yoshie : CANCER-A	ion		519599	6112	2885	300	$\phi \rightarrow \phi$	92	Nω	63	00	0
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	GAATTTGAGGGGTAGAGAAAAGCCTAAGATATACTTTCTACCCTAAAAGCTTCTGTGACA 	TGAGATTTCCTTAAATTGCCAAGCTTTTCCTGGGTTACTTAC	Score 34.8; Pred. No. 0.0 0; Mismatches	c or g or t.		. 7001-730133	01-	US/10/474,495	e et al. ASSOCIATED GENES	10474495	ALIGNMENTS	US-10-41/-3/5A US-10-765-790-	60-550-051-	60-548-091	60-548-091- 60-548-091-	US-60-550-051-3 US-10-796-280-1	10-767-471- 10-796-280-	US-10-767-701- US-10-796-280-	10-796-280- 10-767-701-	-60-545-213- T-US03-35876	-60-545-213-
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	318	103	0 ;									Appl				, P P	•	• •		m .	Αp

RESULT 2
US-60-548-091-5623/c
US-60-548-091-5623/c
; Sequence 5623, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES

THEREOF

FILE REFERENCE: CL001506

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Sequence 12363, Application US/10796280
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: STENOSIS, METHODS OF DE
FILE REFERENCE: CL001510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12363
LENGTH: 304123
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; ORGANISM: Homo sapiens
US-60-548-091-5623
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Matches
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FBStSEQ for Windows Version 4.0
SEQ ID NO 5623
LENGTH: 62555
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SEQ ID NO 1073
LENGTH: 732
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Best Local :
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CURRENT FILING DATE: 2004-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS14784_1
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Cao, Yongwei
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                                                                                                                                  Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
GUNDANOSIS, METHODS OF DETECTION AND U
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                                                                                                                                                   DETECTION AND USES THEREOF
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Query Match

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Score 30.8;

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Length 1647;

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RESULT 6
US-10-767-701-12785
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; LENGTH: 149000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-5666
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US-10-767-701-12785
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                   Sequence 12785, Appl: GENERAL INFORMATION:
                                                                                                         SEQ ID NO 12785
LENGTH: 1647
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                                                                                                                                           APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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CURRENT FILING DATE: 2004-02-27
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                      OTHER INFORMATION: Clone ID:
                                      ORGANISM: Sorghum bicolor FEATURE:
                                                                                       TYPE: DNA
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l Similarity 51.0%;
73; Conservative
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Pred. No. 16;
0; Mismatches
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                  SORBI-28MAY03-CLUS19950_1
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US-10-767-471-10615/c
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; ORGANISM: Homo sapiens
US-10-796-280-12516
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LENGTH: 21872
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US
                                                                                                                             NUMBER OF SEQ ID NOS: 5031
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10615
LENGTH: 1126118
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CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NAME/KEY: misc feature
LOCATION: (1)...(1126118)
OTHER INFORMATION: n = A,
-10-767-471-10615
                                                                                                                                                                                                       APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 6;
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                 or insertion/deletion polymorphism (see Tables 1
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US-10-021-698A-760/c
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US-10-796-280-12479
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LENGTH: 1126118
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                            APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNII
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
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TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: STENOSIS, METHODS OF
                                                                                                                                                                    APPLICANT: KEITH,
APPLICANT: LITTL:
APPLICANT: VAN E
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                      APPLICANT:
CURRENT APPLICATION NUMBER: US/10/021,698A
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ORGANISM: Homo sapiens
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LOCATION: (1)...(11261
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VAN EERDEWEGH, PAUL
DUPUIS, JOSEE
DEL MASTRO, RICHARD
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nilarity 51.9%;
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Pred. No. 46;
0; Mismatches
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DETECTION AND USES THEREOF
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Sequence 34, Application US/10783271
GENERAL INFORMATION:
APPLICANT: Veridex, LLC
APPLICANT: Veridex, LLC
APPLICANT: Wang, Yixin
TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
FILE REFERENCE: VDX-5003 USNP
CURRENT APPLICATION NUMBER: US/10/783,271
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQ ID NO 760
; LENGTH: 8517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-021-698A-760
                                                                                                                                                                                                                                  RESULT 12
US-10-783-271-34/c
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US-10-796-280-12289
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12289
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Best Local (
               SEQ ID NO 34
LENGTH: 175737
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CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: (1)...(663098)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                 OFTWARE: PatentIn version 3.2
TYPE: DNA
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mes 53; Conserv
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58; Conserv
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llarity 55.8%;
Conservative
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 50;
0; Mismatches
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS71888_1 US-10-767-701-4116
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                                                                                                                   Sequence 11693, Application US/10100683
GENERAL INFORMATION:
APPLICANT: ROSEN, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILLNG DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4116
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Best Local (
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LOCATION: (1)..(726)
OTHER INFORMATION: U
FEATURE:
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR APPLICATION NUMBER: US 60/047,601
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TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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Similarity 50.0%;
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Pred. No. 3
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Pred. No. 4;
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FILING DATE: 1997-05-23

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RESULT 15
US-10-796-280-12430/c
US-10-796-280-12430, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; PILE REFERENCE: CL001510
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; LOCATION: (1)...(104403)
; OTHER INFORMATION: n = A,T,C or G,
US-10-796-280-12430
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US-10-100-683-11693
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                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FRANCSC for Windows Version 4.0
SEQ ID NO 12430
LENGTH: 104403
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Best Local Similarity
Matches 64; Conserv
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Best Local Similarity
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FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
94245 TAAGAG 94240
                                                                                   94305 GAAAGAACATTATTCAAAAGTGTGGTAGAAACCTCAGTTAACAGGGAAGAAGATGAAACCT 94246
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4112 CC 4113
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                                         181 CAACAG 186
                                                                                                           | 121 GAAGGTACATTCTGCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGTGGAAAGAC 180
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Pred. No. 46;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS VERSION KEYWORDS SOURCE ORGANISM ACCESSION DEFINITION TITLE JOURNAL Direct Submission
Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9171), Pax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of Library PTB
Unpublished 2 (bases 1 to 658)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y. Pan troglodytes DNA, clone: AG128206 AG128206.1 GI:16657371 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. Pan troglodytes troglodytes (chimpanzee) 658 3 bp DNA PTB-139E19.R, linear GSS 04-NOV-200 genomic survey sequence. GSS 04-NOV-2001

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REFERENCE
AUTHORS
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Ge
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HS_2119_B1_G03_MR CIT Approved Human Genomic Sperm Library
sapiens genomic clone Plate=2119 Col=5 Row=N, genomic surve
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1 (bases 1 to 496)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a:
                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                              Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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'db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                            WA 98109, USA
          Genetics (info@resgen.com).
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g,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ876800 385 bp DNA linear GSS 09-NOV-1999
HS 2114_B2_G08_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2114 Col=16 Row=N, genomic survey
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC end Web Server: http://www.htsc.washington.edu
Plate: 2119 row: N column: 5
                                                                                                                                                                         Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                    Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2114 row: N column: 16
                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 385)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                  Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                       401 Queen Anne Avenue North,
                                                                                                                                                                                                                                                                                                                                                                                                                        10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATATACTTTCTACCCTAAAAGCTTCTGTGACAGCCAAGATGAGCTGTAGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                    quality sequence stop: 385.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT Approved Human Genomic Sperm Library D"/note="Organ; sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                     1. .385
                /clone="Plate=2114 Col=16 Row=N"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="Plate=2119 Col=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:6308280
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_lib="CIT Approved Human Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108.2; DB 2
Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                       Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Row=N"
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  Sperm Library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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PUBMED
REFERENCE
AUTHORS
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VERSION
KEYWORDS
RESULT 5
AY404476
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ORGANISM
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AY404475
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Best Local S
Matches 74
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                               3102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Toodd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 4614)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse ortho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY404475.1
GSS.
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AY404475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                 Similarity
                                                                                   GTCCCAGTTTGAAGGAATGAAGGT 126
                                                                                                                                                      TAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGCGCT:102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCTGTGACAGCCAAGATGAGCTGTAGC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTGTGACAGCCAAGATGAGCTGTAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGTGCTTAGAATTTGAGGGGTAGAGAAAAGCCTAAGATATACTTTCTACCCTAAAAAGC
                                                                                                                                 TAACTTAATGGAATTGAAGTCCTTCCGGACTCTACGAGCACTGAGGCCTCTTCGTGCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTATTGCTTATAATTTGAGGGGTAGAGAAAAGCCTAAGATATACTTTCTACCCTAAAAGC
                                                                GTCCCAGTTTGAAGGAATGAAGGT 3185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 4614)
                                                                                                                                                                                                                                                                                                                                                                                                                     based on alignment
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens SCN11A gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                  locus_tag="HCM1903"
                                                                                                                                                                                                                                                                                                  gene="SCN11A"
                                                                                                                                                                                                                                                                                                                                                                                      .4614
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                                                                                                                                                                                                                13.5%;
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96.6%;
                                                                                                                                                                                                                                                                                                                     .>4614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                Score 46.8; DB 29;
Pred. No. 0.0017;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83.2; DB 28;
Pred. No. 1.2e-15;
O; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4614 bp
, VIRTUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear G
TRANSCRIPT, partial
                                                                                                                                                                                                                            DB 29;
                                                                                                                                                                                                                               Length 4614;
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                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kejariwal, A.,
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                                                                                                                                 3161
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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SOURCE
ORGANISM
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ORGANISM
                                                                                                                                                                                                                                                                                                                                         RESULT 6
CC124756/c
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AUTHORS
                                     JOURNAL COMMENT
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                                                                                                                                                                                                                              KEYWORDS
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                       3159 GCTGTCCCNNTTTGAAGGAATGAAG 3183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3099 CANNNACTTAATGGAATTGAAGTCCTTCCGGACTCTACNNGCACTGAGGCCTCTTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 GCTGTCCCAGTTTGAAGGAATGAAG 124
               1 (bases 1 to 817)
Loftus,B., Shetty,J., Knudson
BAC end sequencing of Aedes a
Unpublished (2003)
Other GSSs: NDL.70A13.T7
Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 CTCTAACTTAATGGAATT--AGAACCTTCCGGATCTACGAGCACTGAGGCCTC-TCGTGC
                                                                                                                                                                                                                                NDL.70Ā13.SP6 Notre Dame Liverpool Aedes NDL.70Ā13, genomic survey sequence. CC124756 CC124756.1 GI:29993811 GSS.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 3772)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,,Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,Adams,M.D. and Cargill,M.
                                                                                                                                                                                                                              GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order them based on alignment.
                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aec
                                                                                                                                                                                      Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene trios
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY404476.1 GI:39760453
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Department of Eukaryotic
                                                                                                                                                                                                          Aedes aegypti (yellow fever mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DN
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCN11A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39.2; DB 29;
Pred. No. 0.46;
0; Mismatches 15;
                                                                                             Knudson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3772 bp
                                                                         aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                             Severson, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas, P., Kejariwal, A.,
                                                                                                                                                                                                                                                                                                       aegypti genomic
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                                                                                                                                                                                                                                                                                                                       Map Building
Unpublished (1997)
Other GSS8: RPCI-11-262E15.TV
Contact: Shaying Zhao, William Nierman, Maper Contact: Shaying Zhao, William Nierman, Maper Contact: Shaying Chac, William Nierman, Maper Contact: Shaying Chac, William Nierman, Maper Contact Shaying Chac, William Nierman, Maper Contact Shaying Contact Sha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 TGÁCCTGCGACCCTGAATCCAGTAGCGCTCGAACTTGATGGGTGTGGCCGCTTTCGGAAC 437
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                                                                                             Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 569)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ487752 569 bp DNA RPCI-11-262E15.TJ RPCI-11 Homo sapiens (RPCI-11-262E15, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
72; Conserv
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Library was provided by David
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AQ487752.1 GI:4673626
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                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
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98: BAC ends
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301-838-0208
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/clone="Vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched Li larvae
by David Severson at the University of Notre Dame and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hongbin Zhang"
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/strain="liverpool"
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62
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                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticum.

1 (Dases 1 to 363)

Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                              Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Miahima, Shizuoka 411-8540, Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in Triticum aestivum 
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ255463.1
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                         GAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTT 192
GTAGTACACTTAATTTACAGGGGAAGAACAACCAACTGAGTTTT 105
                                                               GCATCTGCTGCACTGTTGTAGTTAGGGGGCATGACACTTCTTCCAACAGACGGCATGATA 61
                                                                                              GCCTCTCGTGCGCTGTCCCAGTTTGAAGGAATGAAGGTACATTCTGCAGAAGAATGGGTA 148
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/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1:
/note="Vector: pBACe3.6; Site 1:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7600334"
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                                                                                                                                                                                                           tissue type="spike at flowering date"
/dev_stage="Feekes' scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library,
                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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59.6%;
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395 bp mRNA linear EST 17-SEP-2002
BJ220478 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
CDNA clone wh20e23 3', mRNA sequence.
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Ogihara, Y. and Murai, K.
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EST.
              Tingey, S.V., Powell, W., Wolters, P., Miao, G., Caraher, N. and Hanafey, M.K. DuPont Wheat cDNA Sequence
                                                                                                   pukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                      Triticum aestivum
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5′ end, mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
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                                                                 Pooideae; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                      CACTTCTTCCAACAGACGGCATGATAGTAGTACACTTAATTTACAGGGGAAGAACAACCA
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81-559-81-6855
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/dev_stage="Feekes' scale 9"
/clone_lib="Y. Ogihara unpublished cDNA library,
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/db_xref="taxon:4565"
/clone="wh20e23"
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|mol_type="mRNA"
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                                                  Dolan, M., Hainey, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miao,G., Caraher,N. and Har
DuPont Wheat cDNA Sequence
Unpublished (2002)
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Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
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E. I. DuPont
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Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Innovation Way,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Scott V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 302-631-260
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62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             smail: Scott.V.Tingey@USA.dupont.com
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/tissue type="leaf"
/clone Tib="wlein"
/clone Tib="wlein"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) leaf 7 day old
etiolated seedling (normalized)"
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/db_xref="taxon:4565"
wre1 library"
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/clone_Tib="wrein"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_
/note="Vector: protection of the control 
                                                                                                                                                                                                   /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
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                                                                   AQ931925 448 bp DNA line RPCI-23-282F23.TJ RPCI-23 Mus musculus genomic RPCI-23-282F23, genomic survey sequence.
AQ931925 AQ931925.1 GI:6620939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ240877 Y. Ogihara unpublished cDNA library, Wh_e Triticum aestivum cDNA clone whe17108 3', mRNA sequence.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed genes in Triticum aestivum Unpublished (2002)
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Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BJ240877.1 GI:23083160
                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
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                                                                                                                                                                                                      GTAGTACACTTAATTTACAGGGGAAGAACAACCAACTGAGTTTT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whe17108"
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/dev_stage="Feekes' scale 11.2"
/clone_lib="Y. Ogihara unpublis
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mo
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126 TACATTCTGCAGAAGAATGGGTAGAAGTTCAGTTAACAGAGAAAGGGTGGAAAGACCAACA 185
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                                                                                                                                                                                                                                                                                                                   452 bp mRNA linear wlm96.pk0018.a12 wlm96 Triticum aestivum cDNA clone wlm96.pk0018.a12 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 282 row: F column: 23
Seq primer: SP6
Class: BAC ends.
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1 (bases 1 to 448)
1 (bases 1 to 452)
Tingey, S.V., Powell, W., Wolters, P.,
Miao, G., Caraher, N. and Hanafey, M.K.
DuPont Wheat cDNA Sequence
                                                                                                                                                                                                   Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
DACPAC Resea ch Genetics (info@resgen.com). BAC end page:
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Department of Eukaryotic Genomics
                                                                                                                   Spermatophyta; Magnoliophyta; Pooideae; Triticeae; Triticum.
                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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301 838 0208
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Medical Center Dr., Rockville,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1: /note="Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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'clone="RPCI-23-282F23"
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'strain="C57BL/6J"
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Pred. No. 1.
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                                                            Dolan, M.,
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                                                            Hainey, C., Yuan, Z.
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                          Unpublished (2000)
Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE443872 455 bp mRNA linear EST 25-JUL-2000 WHE1124_E10_J20ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1124_E10_J20, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
                                                                                                     quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (bread wheat)
Triticum aestivum
                                                                                                                                            Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                       Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                   genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGTTCAGTTAACAGAGAAAGGTGGAAAGACCAACAGTTCTTT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCTGCTGCACTGTTGTAGTTAGGGGGGCATGACACTTCTTCCAACAGACGGCATGATA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after
inoculation w/ E. graminis"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4565"
/clone="wlm96.pk0018.a12"
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/clone_lib="wlm96"
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/cultivar="Stephens"
                                           organism="Triticum aestivum"
                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Triticum aestivum"
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clone="WHE1124\_E10\_J20"

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/tissue_type="Root"
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/dev stage="Five day old etiolated seedling"
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library"
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library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
dishes. Roots were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University, Normalization
protocol used was that of Soares. Plasmid DNA
Anderson lab (all other authors)."
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ORIGIN

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                                                                                                                         Query Match
                                                                                                               Local
                  149 GAAGTTCAGTTAACAGAGAAAAGGTGGAAAGACCAACAGTTCTTT 192
                                               398 GCATCTGCTGCACTGTTGTAGTTAGGGGGGCATGACACTTCTTCCAACAGACGGCATGATA
                                                                  89 GCCTCTCGTGCGCTGTCCCAGTTTGAAGGAATGAAGGTACATTCTGCAGAAGAATGGGTA 148
                                                                                                  62;
                                                                                                             Similarity
GTAGTACACTTAATTTACAGGGGAAGAACAACCAACTGAGTTTT
                                                                                                  Conservative
                                                                                                             10.6%;
59.6%;
                                                                                                0;
                                                                                                             Score 36.8; D. Pred. No. 1.2;
                                                                                                  Mismatches
                                                                                                                         DB
                                                                                                  42;
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                                                                                                                         Length 455;
  295
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Search completed: March 22, 2004, 23:12:35
Job time : 2045.07 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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223
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SUMMARIES

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### ALIGNMENTS

TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX017229	RESULT 1
Mammalian sodium channel proteins Patent: WO 9947670-A 13 23-SEP-1999;	Tate, S.N., Grose, D.T. and Hick, C.A.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX017229.1 GI:10042149	AX017229	Sequence 13 from Patent WO9947670.	AX017229 223 bp DNA linear PAT 07-SEP-2000		

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RESULT 2
BD138451
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 223)

Grose,D.T., Hick,C.A. and Tate,S.N.
Mammalian sodium channel protein
Patent; JP 2002508941-A 12 26-MAR-2002;
                                                                                                                                                                                                                                                 PC C12N1/19, C12N1/21, C12N5/10, C12Q1/02, G01N33/15, G01N33/50, G01N33/ PC
                                                                                                                                                                                                                                                                                  PD 26-MAR-2002

PF 18-MAR-1999 JP 2000536853

PR 18-MAR-1998 GB 9805793.8

PR 10-MAR THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE

C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, P

C12N1/15,
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JP 2002508941-A/12.
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100.0%; ilarity 100.0%; Conservative 0;
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Location/Qualifiers
                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 6.4e-51;
; Mismatches 0;
Score 223; DB 6;
Pred. No. 6.4e-51;
Mismatches 0;
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                                                                                                                                                                                                                                                                  Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 167476) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Phelps, K.A., Buckley, D.,
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Kaul, R.K., Olson, M.V.,
Direct Submission
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4 (bases 1 to 167476)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-2002) Genome Box 352145, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Haugen, E.D.
Direct Submission
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Kaul, R.K., Olson, M.V., Zhou, Y.,
Saenphimmachak, C., Buckley, D.,
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Mammalia; Eutheria;
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                            Chemistry: Dye-terminator ET; 45% of reads Chemistry: Dye-terminator Big Dye; 55% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 167476 bases at least Q40
Consensus quality: 167476 bases at least Q20
Consensus quality: 167476 bases at least Q20
                                                                                                                                     Center clone name: RP11-134J21 (bc0780)
------ Summary Statistics
Sequencing vector: plasmid; 100% of reads
                                                                                                                                                                                                             Contact: uwgchtgs@u.washington.edu
----- Project Information
                                                                                                                                                                                                                                                              Center: University of Washington Genome Center Center Code: UWGC
                                                                                                                                                                                                                                               Web site: http://www.genome.washington.edu
Insert size: 167476; sum-of-contigs
Quality coverage: 18.9x in Q20 bases; sum-of-contigs
                                                                                                                                                                                           Center project name: chr-3
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Kibukawa, M.,
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Raymond, C.
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553	3049  762	687	3468	4710	6640	72	4175	72	245	3455	4889	2016	9345	2248				sequermap	BCORL	fragments	in the tab	vector, in Small frag	The electr	This seque fingerprin	Sequence Validation:	covered by subclone; a	problems, such	alternate c	This sequen	but are av	Quality le 1 error in	This entry	Sequence Qu	S': RP	Orner Tanning
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8072	1891	7123	179	727	4721	3014		1364	5818	184	4809	2707	449	512	0300		31	sequermap	Hindii	ited by dashe	are no signi	accurately r w a variable	ince-predicte	en validated		one plasmid s sembly was co	pressions an	or covered by	nished as fol	part of thi	. Base-by-b	This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.	ssment:	AC137625, 20 (UWGC:bc0782	
8171	1888	7158	<b>&lt;800</b>	745	4667	3028	.990	1346	5899	<800	4878	2741	<800	<b>&lt;</b> 800	. 6014		224	FngrPrnt		dicted va	ficant re	epresent	ence cons	e experim	•	nfirmed b	de to res d repeats	high qua	lows unle	s entry's	ected to h	th sequen		01-bp ove	
4636	6949	2550	2649	4704	2738	8136	2583	4036	2486	1923	2537	2813	2317	5097	2067		.I.	Sequermap	Bglii	lues. Unique	maining disci	vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp)	ists of both	ple Complete entally deriv		y at least one plasmid subclone or more than one M13 and the assembly was confirmed by restriction digest	; all regions	all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Ph	sequence was finished as follows unless otherwise noted:	ASN.1 file.	Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are	nce quality program.		3': RP11-1114A3 AC137625, 2001-bp overlap 3': RP11-12A24 (UWGC:bc0782) AC123903, 41341-bp overlap	
4629	4862 6960	2550	2744	4629	2744	8039	2550	3992	2550	2008	2550	2744	2259	5007	2008	2 6	သ က စ	FngrPrnt		ly ordered	repancies	ircular BAC. Y 400-800 bp	insert and	Digest ved digest	•	one M13 n digest.	s were	e., Phred	noted:	30	o p			overlap	
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5397 <800	1068	2040	6824	1555	<b>^800</b>	<800	7557	1188	3639	4430	1346	<b>&lt;800</b>	2040	4039	<800	1188	3639	<800	<800	5089	2371	<800	5397	1408	<800	1228	5397	<800	3264	1068	4878	<800	5397	3639	
4788 4058	4811	252	3630	4557	1242	253	3335	2731	6314	344	1967	1198	161	317	879	4240	14	2486	4714	396	4232	790	3725	2044	1294	4079	3022	694	1222	178	4728	953	5748	604	2 1 1 2 2

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Best Local Similarity
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Matches 143; Conserv
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PC C12N15/
C12P21/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 856)

Paul, S.D., Linda, M.F., Rina, K., Douglas, K.R. and Laksmi, S. Nucleic acid encoding sodium channel of nerve tissue Patent: JP 19925186-A 2 31-AUG-1999; F HOFFMANN LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E36123
Nucleic acid encoding
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DOUGLAS KENESU RAMBERT,
PI LAKSMI SANGEIMUSUWARAN
                                                        AAGGTGGTGATCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGACT 105465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTA 133
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JP 1999235186-A/2
                                                                                          Conservative
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20-NOV-1998 JP 1998331769
20-NOV-1997 US 60/066225
                                                                                                                                                                                                                                                                                           C12Q1/68,G01N33/53,G01N33/577,G01N33/68//(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,C12N5/00,
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                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.3e-23;
0; Mismatches 7
                                                                                       Score 107.8; DB 6;
Pred. No. 3.7e-19;
0; Mismatches 2;
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channel of nerve
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                                                                                                                                                                                                                   sapiens (human)'
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rve tissue.
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                                                                                          Indels
                                                                                                              Length 856;
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2896 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT
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AR340648
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Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal root ganglia
Patent: US 6573067-A 6 03-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                                                                                                                           Regulation of sodium channel BD217793 GI:33027563
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Hajj,S.D. and Waxman,S.
Regulation of sodium channel in posterior
Patent: JP 2002509860-A 3 02-APR-2002;
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                 JP 2002509860-A/3.
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n patent US 657<sup>2</sup>
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Primates;
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Matches 143; Conserv
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5728)
Kanazawa, I., Goto, J. and Jeong, S.Y.
Human sodium channel SCN12A and SCN8A
Patent: WO 0190355-A 2 29-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                            JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON
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WO 0190355-A/2.
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              CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
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CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA
                                                     AAGGTGGTGGTCAATGCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT
                                                                    AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT
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llarity 96.0%;
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llarity 96.0%;
Conservative
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23-MAY-2000 JP 00P 152085
ICHIRO KANAZAWA, JUN GOTO, SEON
C12N15/12, C07K14/47, C07K16/18
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WO 0190355-A/2
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Location/Qualifiers
                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 3.5e-19;
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Pred. No. 3.6e-19;
0; Mismatches 2
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JOURNAL
MEDLINE
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BD082952
BD082952.1
                                                                                                                                                                                                           5728 bp mRNA linear PRI Homo sapiens voltage-gated sodium channel alpha subunit, splice variant SCN12A-s (SCN12A) mRNA, complete cds. AF150882
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 5728)

Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.

Identification of a novel human voltage-gated wadium channel alphisubunit gene, SCN12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanazawa, I., Goto, J. and Tei, Y.

Human sodium channel SCN12A
Patent: JP 2001377294-A 2 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
P 2001327394-A/2
PN JP 2001327394-A/2
PD 27-NOV-2001
PD 27-NOV-2001
PF 23-MAY-2000 JP 200152085
PI ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
PC C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
             subunit gene, SCN12A
Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
                                                                                                                                               Homo sapiens
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1 (bases 1 to 5728)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                               GI:6693704
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Pred. No. 3.5e-19;
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Best Local Similarity
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Jeong, S.-Y., Suzuki, T., Hashida, H., Ogata, K., Masuda, M., Goto, Jand Kanazawa, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-MAY-1999) Neurology, Graduate School of Medicine Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tokyo 113-8655, Japan
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                                                                                                                                                 TTTGGGAAATGCATT-AATGGAACAGACT 3836
                                                                                                                                                                                        TTTGGGAAATGCATTCAATGGAACAGACT 200
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PTVSCLRHWHMCDFWHSTLVVFRILCGEMIENMECMQEANASSSLCVIVFILTITVIG
KLVVLNLFIALLLNSSENEENKGNLEGGEAFKVQLALDFRREAFCFVRHTLEHFFVHK
WCRKQNLPQQKEVAGGCAAQSKDIIFLVMEMKRGSETQEELGILTSVPKTLGVRHDWT
WLAPLABEEDDVEFSGEDNAQRITQPEBEGQAYELHQENKKFGSRCVQSVEIDWFSED
EPHLTIQDFRKKSDVTSILSEGSTIDLODGFGWLEBWFVEKQPERCLFRFGCFCFCC
EPHLTIQDFRKKSDVTSILSEGSTIDLODGFGWLEBWFVEKQPERCLFRFGCFCFCC
EVDKRKPPWVIWMNLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDWHLENQPKIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
RTLRALRPLRALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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HFDEHGDPLQKQRALSAVSILTITMKEGEKGLECHCFGCSHLASKYLVMNCCPQHLCV
KKVLKTVMTDDPTELAITICIIINTVELAMEHKMEASFEKMLNIGNLVPTSIFJAEN
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
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FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
IAECVFTGIYIFEALIKILARGFILDEFSFLRDPWNWLDSIVIGIAIVSYIPGITIKL
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/protein_id="AAF24980.1"
/db xref="GI:6693705"
/translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT
                     41 from patent
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NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
VLLSIVSK"
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/chromosome="3"
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Pred. No. 3.5e-19;
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Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal root ganglia
Patent: US 6573067-A 41 03-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A, Submitted (25-SEP-1999) Neurology, Yale University/VAMC, 127A, Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 6237)
Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman,S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ganglion neurons FEBS Lett. 462 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two tetrodotoxin-resistant sodium channels in human dorsal root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 6237)
Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="SCN11A"
/note="NaN alpha :
/codon_start=1
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/mol_type="genomic DNA"
                                                                         /gene="SCN11A"
                                                                                                                            'gene="SCN11A"
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chromosome="3"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                               issue_type="dorsal root ganglia"
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Pred. No. 3.5e-19;
0; Mismatches 2
                         subunit; TTX-R sodium channel"
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/product="voltage-gated sodium channel type XI alpha

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RESULT 12
BD012082
                                                                      KEYWORDS
                                                                                            VERSION
                                                                                                                    ACCESSION
                                                                                                                                          DEFINITION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                     Homo sapiens (human)
                                                                 BD012082.1 GI:22092271 WO 0190355-A/1.
                                                                                                                  Human sodium channel SCN12A BD012082
                                                                                                                                                                BD012082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                TTTGGGAAATGCATT-AATGGAACAGACT 3667
                                                                                                                                                                                                                                                                                                                           TTTGGGAAATGCATTCAATGGAACAGACT 200
                                                                                                                                                                                                                                                                                                                                                                         CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA
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LLNCTDJIFTHIFILEWYLKWVAFGFGKYFTSARCCLDFIIVIVSVTTLJILMELKSF
RTLRALRPLRALSQFESKVIVNALIGAIPALINVLLVCLIFWLVFCTIGVYFETSKF
GKCINGTDSVINYTIITMKSQCESGNFSWINQKNNFDNVGNAYLALLQVATFKGMDI
IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNFIGVIINMFNQQKKLGG
DIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKCQGLVFDIVTSQIFDIIISISLIIL
NMISMAESYNQPKANKSILDHLMWVFVVIFTLECLIKIFALRQYYFTMMNLFDVV
VLLSIVSTMISTLENQEHIPFPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
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HFDEHGDPLQRQRALSAVSILTITMKEQEKSQEPCLPCGENLASKYLVMNCCPQWLCV
KKVLRTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCN11A"
5689. .5961
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WLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKPTSQRVQSVEIDMFSED
EPHLTIQDPRKKSDVTSILSECSTIDLQDGFGWLPEMVPKKQPERCLPKGFGCCFPCC
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PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENMWECMQEANASSSLCVIVFILITVIG
KLVVLNLFIALLLNSFSNEERNGNLEGEARKTKVQLALDRFRRAFCFVRHTLEHFCHK
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PDYNYTNFDNPGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFPFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT
GEVPQDFXPADSKLPKLYGDIPRELIGKELEDLDPFYRNHKTFMVLNRKRTIYD
FSAKHALFIFDFFNSIRSLAIRVSVHSLFSMFIGTVIINCVFWATGPAKNSNNSNN
IABCVFTGIYIFEALIKILARGFILDEFSFLRDPWNWLDSIVIGIAIVSYIPGITIKL
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WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
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/db_xref="GI:6572950"
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/note="polyA_signal"
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96.0%;
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                                                                                                                                          SCN8A.
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BD082951
LOCUS
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ORGANISM
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ACCESSION
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Matches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6528)
                                                                                                                                                                                                                                                                                                                                                                                                   Human sodium channel SCN12A.
BD082951
BD082951.1 GI:22628561
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Human sodium channel SCN12A and SCN8A
Patent: WO 0190355-A 1 29-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,ICHIRO KANAZAWA,JUN GOTO,
                                                                                   Patent: JP 2001327294-A 1 27-NOV-
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                   Kanazawa, I., Goto, J. and Tei, Y. Human sodium channel SCN12A
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                 JP 2001327294-A/1
27-NOV-2001
23-MAY-2000 JP 2000152085
ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
                                                                                   CDS
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23-MAY 2000 JP 00P 152085
ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
C12N15/12, C07K14/47, C07K16/18
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WO 0190355-A/1
29-NOV-2001
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                                                            Location/Qualifiers (200). .(5575). Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Pred. No. 3.5e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6528)

3 deong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.

1 Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens voltage-gated sodiu (SCN12A) mRNA, complete cds. AF109737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 6528)
Jeong, S.Y., Suzuki, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-NOV-1998) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit gene, SCN12A
Biochem. Biophys. Res. Commun. 267 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF109737.1 GI:6693696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanazawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGGAAATGCATT-AATGGAACAGACT 3836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA 3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT 3750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGGGAAATGCATTCAATGGAACAGACT 200
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                                         /translation="MDDRCYPVIFPDERNFFPFTSDSLAAIEKRIAIQKEKKKSKDQT
GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNKTPMVLNRKGTIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIJGTVIINCVPMATGPAKNSKUPKTYGDIFT
IABCVFTGYIIFEALIKILARGFILDEFSFLRDPMNNLDSIVJGIAIVSVJFGTIKL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIMMGNSACSIQYECKHTKIN
DYNYTNFDNFGMSFLAMFRLMTQDSWELTYQQTLFTTGLYSVFFFIVVIFLGSFYLI
NLTLAVTMAYEEQNKKVAABIEAKEKMFQEAQQLLKEKEALVAMGIDRSSLTSLET
SYFTPKKRKLFGNKKKSFFLRESGKDQPFGSDSDEDCQKFQLLEQTKRLSQNLSLD
HFDEHGDPLQRQRALSAVSILTITMKEQEKSQBFCLPGGENLASKYLVMNCCPQMLCV
HFDEHGDPLQRQRALSAVSILTITMKEQEKSQBFCLPGGENLASKYLVMNCCPQMLCV
KKVLRTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
                                                                                                                                                                                                                                                                                                                                                 /product="voltage-gated sodium channel alpha subunit SCN12A"
                                                                                                                                                                                                                                                                                             /protein_id="AAF24976.1"
/db_xref="GI:6693697"
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCN12A"
                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="SCN12A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             map="3p21.3-p23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suzuki, T., Hashida, H., Masuda, N., Goto, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.3%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107.8; | Pred. No. 3.5e | 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA linear PRI 15-JAN-
channel alpha subunit SCN12A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262-270 (2000)
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PITVSCLRHWHMGDFWHSFLVVFRILLGEWIENMWECMQBANASSSLCVI VFILITVIG
KLVVLNLFIALLLNSFSNEERNGNLEGEARTKYKVQLALDFRRAFCFVRHTLEHCHK
WCRKQNLDQKEYNGGCAAQSKDII PLYMEMKRGSETQEELGILTSVBKTLGYBHDWT
WLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKPTSQRVQSVEIDMFSED
EPHLTIQDPKKSDVTSILSECSTIDLQDGFWLPENVFKKQPERCLFWGFGCCFPC
SVDKRKPDWVIWMLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVHLENQPKIQE
LLMCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVVSTTLINLMELKSF
RTIRALRERALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCTLGVYFFSGKF
GKCINGTDSVINYTIITNKSQCESGRFSWINQKVNEDVGNAYLALLQVATFKGMDI
IYAAVDSTEXEQQDFESMSLGYIYVVPILFGSFFTLNLFIGVIINDKNQQXKLIGG
QDIFMTEEQKKYYNAMKKLGSKKPQKFIFPLECLIKIFALLRCYYFTNGWNLFDCVV
VLLSIVSTMISTLENGEHTPFPTLFRIVRTLECLIKIFALAGYYFTNGWNLFDCVV
VLLSIVSTMISTLENGEHTPFPTLFRIVRTHAFTIGHILTVRAARGIRTLLFALMMSL
PSLFNIGLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSMLCLFQISTSAG
WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIISFLIVNMYIAVILENFWTA
TEESEDPLGEDDFDIFTYEVWEKFDFEATQFIKYSALSDFADALFEELRVAKFMKXQFL
VNDLFMVSSDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
TTKRKEEERGAAIIQKAFRKYMKVTKGDQGDQNDLENGPHSPLQTLCNGDLSSFGVA
KGKVHCD"
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ORIGIN

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REFERENCE
AUTHORS
TITLE
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AUTHORS
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ORGANISM
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HSA417790
LOCUS
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VERSION
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                                                                                                                                                                                                                                                               JOURNAL
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                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                   Submitted (25-OCT-2001) Blum R.,
Ludwig-Maximillians-Universitaet,
608, 80802 Muenchen, GERMANY
                                                                                                                                                                                                                                                  Nature 419
22272672
                                                                                                                                                                                                                                                                                                         Blum, R.,
                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      NAV1.9 gene; voltage-gated sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens mRNA for voltage-gated sodium
                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                            Na (V) 1.9
                                                                                                                                                                                                                                                                                            Neurotrophin-evoked depolarization
                                                                                                                                                                                                                                                                                                                                                                                                       AJ417790.1 GI:22796539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                     .2384689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGGTGGTGGTCAATACCTCTCATAAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGGGAAATGCATT-AATGGAACAGACT 3836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGGGAAATGCATTCAATGGAACAGACT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                      (bases 1 to 5419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/cell_line="SH-SY5Y"
                                                                                                                                                                                                                                                                                                         Kafitz, K.W.
           /gene="NAV1.9"
1. .5376
                                                                                                                                     Location/Qualifiers
'gene="NAV1.9"
                                                      Cell
                                                                                                                                                                                                                                                                 (6908),
                                         .5419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%;
                                                    type="neuroblastoma"
                                                                                                                                                                                                                                                                  687-693 (2002)
                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107.8;
Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                         and Konnerth, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                5419 bp
                                                                                                                                                                                                                                                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                 Institut fuer Physiologie,
, Biedersteiner Strasse 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5e-19;
                                                                                                                                                                                                                                                                                              requires the sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 09-OCT-2002 (NAV1.9 gene).
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                                                                                                                                                                      Geb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3750
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Search completed: March 22, 2004, 19:32:33 Job time: 1190.12 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                3610
                                                                                                                                                                                                                                                        3552 CTGCCTTATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA 3609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          52 AAGGTGGTCGATCCTCCATAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                         CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                             TTTGGGAAATGCATT-AATGGAACAGACT 3637
                                                                                                                                                                  TTTGGGAAATGCATTCAATGGAACAGACT 200
                                                                                                                                                                                                                                                                                                                                                                                  AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT 3551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
NITLAVUTMAYEEQNKNVAABI EAKEKMFQBAQQLLKEEKBALUAMGI DRSSLTSLET
SYFTEKKRKLFGNKKRKSFFLRESGKDQPFGSDDEDCKKPQLLEGTKRLSQNLSLD
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KKVLRTVMTGFFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWFPLRSFRVLRVFKLAK
SWFTLMTLKIIGNSVGALGSLTVULVIFIFSVVGMQLFGRSFRSQKKSPKLCWFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GOA:Q8NDX3"
/db_xref="GOA:Q8NDX3"
/db_xref="SPTREMEL:Q8NDX3"
/cranslat.on="ModRCYPVIFPDERNFRPPTSDSLAAIEKRIAIQKEKKXSKDQT
/cranslat.on="ModRCYPVIFPDERNFRPPTSDSLAAIEKRIAIQKEKKXSKDQT
GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYNHKTFWVLNRKRTIYR
FSAKHALF!FGDFNSIRSLAIRVSVHSLFSMFIIGTVINCVFMATGBAKNSNSNNTD
IAECVFTGIYIFEBALIKILARGFILDEFSFLEDPMNMLDSIVIGIAIVSY!FGAIKLL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKFTSQRVQSVEIDMFSED
EPHLTIQPERKKSDVTSILSECSTIDLQDGFGWLPEMVPKKQPERCLPKGFGCCFPCC
SUDKRKPPWINMALRKTCYQIVKBSWFESFIIFUILLSGGALIFEDWHLENQPKIQE
LLNCTDIIFTHIFILEMVLKMVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTKRKEEERGAAIIQKAFRKYMMKVTKGDQGDQNDLENGPHSPLQTLCNGDLSSFGVA
KGKVHCD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENMWECMQEANASSSLCVIVFILITVIG
KLVVLNLFIALLLNSFSNEERNGNLEGEARKTKVQLALDRFRRAFCFVGHTLEHFCHK
WCRKQNLPQQKEVAGGCAAQSKDIIPLVMEMKRGSETQEELGILTSVPKTLGVRHDWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   excitation"
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'protein_id="CAD10507.1"
'db_xref="GI:22796540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="mediates neurotrophin-evoked neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.6%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106.2; DB 9; Length 5419; Pred. No. 9.8e-19; 0; Mismatches 3; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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Maximum
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic
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### ALIGNMENTS

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Query Match
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Matches 223
                                                                                       AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a
                                                                                                                                                                                                                                                                                                                                                                                                                              Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
                                                   Sequence 223 BP; 41 A; 50 C; 44 G; 88 T; 0 U; 0 Other;
                                                                                                                                                                     Claim
                                                                                                                                                                                              Mammalian sodium channel protein for treating pain and hypersensitivity
                                                                                                                                                                                                                        WPI; 1999-562112/47.
                                                                                                                                                                                                                                                  Grose
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sensory neurone specific 2a nucleotide sequence fragment #11
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                                                                             medicament
                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                    18-MAR-1998;
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                                                                                                                                                                                                                                                  DT,
                                                                                                                                                                    6; Page 67; 73pp; English.
                                                                                                                                                                                                                                               Hick CA,
                                                                             for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
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100.0%; Score 223; DB 2;
100.0%; Pred. No. 6.1e-54;
Live 0; Mismatches 0;
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                                                                                                                                  Query Match
                                                                                                                                                                                     The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3A; 90pp; French.
                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY16577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dorsal root ganglia; tetrodotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Type 5 sodium channel; PN5; nervous system; plexiform;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                     Local Similarity
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CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                     DNA encoding sodium channel of the nervous system
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                                                               AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                                                             856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCATTCAATGGAACAGACTTTTAGGAATTTCCAGCGATTCCT 223
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                                                                                                                   Score 107.8; DB 2; Pred. No. 6.9e-21;
                                                                                                      Mismatches
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                                                                                                                                                                       Matches
                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                             Sequence 3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                       modifying the behaviour or these weave wear mener is named SCN11a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 8A1-2; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
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                                                                                                                                                                                          Local
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                                                                                                                                                                                          Similarity
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CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                    AAGGTGGTGGTCAATACCTCTCATAAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
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                                                                                                                                                                       Conservative
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98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US002008
                                                                                                                                                                                          48.3%;
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                          Score 107.8; DB Pred. No. 1e-20;
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                                                                                                                                                                                                             DB 2;
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                                                                                            CC CDNA was isolated from a human dorsal root ganglia tissue cDNA library by CC PCR amplification (see also AAF30122-23). A full-length sequence is given CC in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium CC channel protein family and produces a TTX-R sodium current. Such channels CC underlie the generation and propagation of impulses in excitable cells CC such as neurons and muscle fibres. Preferential expression of NaN on CC sensory neurons innervating the body (dorsal root ganglia) and the face CC (trigeminal ganglia), but not on other neurons, makes it a very useful CC target for diagnostic and/or therapeutic uses in relation to acute and/or CC chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves CC administering an agent that alters sodium current flow through NaN CC channels, or which modulates transcription or translation of NaN mENA, in CC channels, or which modulates transcription or translation are used in CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in CC channel expression or (antisense) to down-regulate NaN expression, in the CC channels of disease, and in the recombinant production of NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a partial cDNA for a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 8A; 162pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sodium channel NaN partial cDNA
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB20125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-103147/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGAGTATACTTC--TTTTCTGGAAAA 2949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGGGAAATGCATT-AATGGAACAGACT
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   BP;
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1. .3699
       1043 A; 807
   C; 820 G; 1030 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2977
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Query Match Best Local Similarity

48.3%; 96.0%;

Score 107.8; Pred. No. 1e-

DB 4;

Length 3701;

Query Match Best Local Similarity

48.3%; 96.0%;

Score 107.8; DB 6; Pred. No. 1.2e-20;

Sequence

5728

B₽;

1637 A; 1241 C; 1199 G; 1650 T;

0 U; 1 Other;

Length 5728;

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Matches
                                        The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present CDNA sequence encodes the human SCN12A-s sodium channel
                                                                                                                                                                                                                                   Sodium channel alpha subunits SCN12A and SCN8A of human nervous stogether with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; human nervous system; chromosome 3p23-21.3; excitatory cell; drug development; familial hyperglycaemia; QT extending syndrome type 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL42750 standard; cDNA;
                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL42750;
                                                                                                                                                                                                      Claim 7; Page 55-70; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                 Kanazawa I,
                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2000; 2000JP-00152085
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                                                                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sodium channel subunit SCN12A-s coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AAGGTGGTGAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT
                                                                                                                                                                                                                                                                                                   AA014926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGGGAAATGCATT-AATGGAACAGACT 3040
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                                                                                                                                                                                                                                                                                                                                                 Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Human sodium channel subunit SCN12A-s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Jeong
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                           The present sequence is that of cDNA encoding a novel human tetrodotoxin CC resistant sodium channel, termed NAN (see AAB20121). The cDNA was cisolated from a human dorsal root ganglia tissue cDNA library by PCR CC isolated from a human dorsal root ganglia tissue cDNA library by PCR CC amplification (see also AAB20122-23). NAN belongs to the a-subunit CC voltage-gated sodium channel protein family and produces a TTX-R sodium CC current. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres. CC Preferential expression of NAN on sensory neurons innervating the body CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed CC method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NAN channels, or which modulates cranscription or translation of NAN mENA, in dorsal root ganglia or trigeminal neurons. NAN nucleic acids are used in gene therapy to correct disjorders associated with decreased sodium channel expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 11A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dib-Најј S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-US019342
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                     The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein
                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                             Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant.
                               Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence encodes a numan Na V 1.9 souther challent is used in the exemplification of the present invention.
                                                                                                             P-PSDB; AAO14925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human nervous
                                                                                                                                                                                                      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; n nervous system; chromosome 3p23-21.3; excitatory cell; development; familial hyperglycaemia; QT extending syndrome type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3582
                                                                                                                              2002-393394/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endplate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sodium channel subunit SCN12A coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTTCCTGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGTGGTGATCAATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGGGAAATGCATTCAATGGAACAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGGGAAATGCATT-AATGGAACAGACT 3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                 Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                 200. .5575
                                                                                                                                                                                                                                                                                                                                                                                            /product= "Human sodium channel subunit SCN12A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                   Jeong
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Pred. No. 1.2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5860;
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6; Page 29-46; 118pp; Japanese

Ś 문 S 밁 S

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RESULT 9
AAX87601
ID AAX8
XX AAX8
AC AAX8
AC AAX8
DT 26-O
XX MOUS
XX MOUS
XX MUS
XX PT CDS
FT CDS
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FT W095
XX W095

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Best Local &
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                                                                                                                                                                                     29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NaN; sodium channel; ion transport; mouse; dorsal root paraesthesia; hyperexcitability; therapy; Scnlla gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX87601 standard; cDNA; 5822
                                WPI; 1999-479168/40.
                                                                               Dib-Hajj
                                                                                                                                                                                                                                                                                                                        05-AUG-1999
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                                                                                                                                   (UYYA ) UNIV
                                                                                                                                                                                                                                                                 29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                            WO9938889-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143;
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                                                                                                                                                                                     98US-0072990P
98US-0109402P
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4201. .4260
                                                                                                                                                                                                                                                                 99WO-US002008
                                                                                                                                                                                                                                                                                                                                                                                                                              5789. .5794
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "these bases represent nucleotides missing from the sequence given in Fig 7 of the specification. The nucleotides are included to maintain the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numbering given in the sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19. .5316
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Pred. No. 1.2e-20;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the nucleotide for this DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ganglia; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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RESULT 10
AAF30103
ID AAF30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat NaN-based primers (see AAX87618-19). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA agents that modulate NaN channel activity or NaN channel mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of Nau in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The gene encoding NaN has been named Scnlla
                                                                                                                                                                                                                                                                                                   Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; paraesthesia; hyperexcitability; analgesic; vaccine; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated products for
                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                    diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF30103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF30103 standard; cDNA; 5822 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 0 U; 61 Other;
 14-JUL-2000; 2000WO-US019342
                                     25-JAN-2001.
                                                                      WO200105831-A1
                                                                                                                      polyA_site
                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                             Mouse sodium channel NaN cDNA.
                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 37.5%;
Local Similarity 82.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGGAAGATGCATT-AATGGAACAGACATAAATAATAT 3603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCTCATTTTCTGGCTCATATTTTGTATCCTGGGAGTAAATTT--TTTTTCTGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGTTGTTGTCAATGCCCTCATGAGTGCCATACCTGCCA-TCCTCAATGTCTTGCTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids encoding sodium channels, used to develop treating acute or chronic pain or hyperexcitability
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                                                                                                                                       5789. .5794
/*tag= b
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/= c
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Pred. No. 9.6e-14;
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                                                                                                                                                                                                                                                                                                         therapy;
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                                                                                                                                                                                                                                                                                                                            pain;
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RESULT 11
ADD32195
ID ADD32
XX ADD32
AC ADD32
XX IS-UB
AC ADD32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 7A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                 expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron
                                                                                                                                                                                                                                      Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535
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                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                        15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                       ADD32195;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD32195 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%;
Similarity 82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGITGITGICAATGCCCTCATGAGTGCCATACCTGCCA-TCCTCAATGTCTTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGGAAGATGCATT-AATGGAACAGACATAAATAATAT 3603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGGGAAATGCATTCAATGGAACAGACTTTTAGGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCTCATTTTCTGGCTCATATTTTGTATCCTGGGAGTAAATTT--TTTTTCTGGGAAG
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                                                                                                                                                                                                                                                                                                        (first entry
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   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.6; DB 4;
Pred. No. 9.6e-14;
0; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
                                                                                                                                        mouse; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse tetrodotoxin
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3564

WO2003080570-A2.

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/\*tag= a /product= 19. .5316

"Na v 1.9 sodium channel protein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell of sodium current is indicative of an agent capable of modulating sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (4) a recombinant capable of modulating sodium current in a cell; and (5) a method to the second under the cell; and (6) a recombinant capable of modulating sodium current in a cell; and (6) a recombinant capable of modulating sodium current in a cell; and (6) a recombinant capable of modulating sodium current in a cell; and (6) a recombinant capable of modulating sodium current in a cell; and (7) a sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant capable of modulating sodium current in a cell; and (8) a recombinant 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a mouse Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vector useful for stable cloning and expression of Navl.9 sodium channel at the mRNA and protein levels comprises a nucleic acsequence that encodes a mammalian Navl.9 sodium channel protein or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-876895/81.
P-PSDB; ADD32196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-2002; 2002US-0365550P
                          ADD32209
                                                                               ADD32209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or
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                                                                                                                                                                                                                                                                                                                                       3507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                               standard; cDNA; 5298
                                                                                                                                                                                                                                                                                                                                       CTGCCTCATTTTCTGGCTCATATTTTTGTATCCTGGGAGTAAATTT--TTTTTCTGGGAAG 3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGGTTGTTGTCAATGCCCTCATGAGTGCCATACCTGCCA-TCCTCAATGTCTTGCTGGT
                                                                                                                                                                                                                       TTTGGAAGATGCATT-AATGGAACAGACATAAATAATAT 3603
                                                                                                                                                                                                                                                                                                                                                                                             CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                         TTTGGGAAATGCATTCAATGGAACAGACTTTTAGGAATTT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greenwood JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83.6; DB 9;
Pred. No. 9.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
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TTTGGGAAATGCATTCAATGGA 193

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                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                             The present invention describes an expression vector comprising a nucleic classid sequence that encodes a manmalian Na v.1.9 sodium channel protein or cits fragment, and producing a sodium current when transfected in a cell. CC Also described: (1) a recombinant cell comprising the plasmid selected cC from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v.1.9 cC sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell cunder conditions that allow expression of Na v.1.9 sodium channel protein cc produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an cc alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cc capable of modulating sodium current in a cell; and (4) a recombinant cc cell comprising the expression vector. The expression vectors are useful cfor the stable cloning and expression of the Na v 1.9 sodium channel at cc the mRNA and protein levels, and for producing sodium channel currents cc characteristic of native currents in dorsal root ganglion neurons. The cresent sequence encodes a rat Na v 1.9 sodium channel protein, which is cused in the exemplification of the present invention.
                                                                                                                                                                 Matches
                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cbs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Na v 1.9
                                                                                                                                                                                                                                               Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-876895/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gonda MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2003; 2003WO-US008611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression vector; Na v 1.9 sodium channel protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TRAN-) TRANSMOLECULAR INC.
3486
                                                                                                                                                               112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channel protein; dorsal root ganglion neuron; rat; gene; ss.
                                                                                                                                                                                     Similarity
                              CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTTCCTGGAAAA 171
CTGCCTCATTTTCTGGCTCGTATTTTGTATCTTGGGAGTAAATTT--ATTTTCTGGGAAG 3543
                                                                               AAGGTTGTCGTCTÁCGCCCTGÁTCAGCGCCÁTÁCCTGCCÁTT-CTCÁATGTCTTGCTGGT
                                                                                                                      AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 19; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sodium channel protein encoding cDNA SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                   32.6%;
78.9%;
                                                                                                                                                                 0
                                                                                                                                                                                                      Score 72.8; DB 9;
                                                                                                                                                                                     Pred.
                                                                                                                                                                 Mismatches
                                                                                                                                                               No. 1.1e-10; amatches 27;
                                                                                                                                                                                                        Length 5298;
                                                                                                                                                                 Indels
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RESULT 14
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 112; Conserva
                                                                                                                                                                                                                                                                                                                                              The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy; neuropathic pain; migraine; headache; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX60244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-315739/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stabilised cDNA encoding type 5 sodium channel protein designated PN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX60244 standard; cDNA;
               AAX87600;
                                      AAX87600 standard;
                                                                                                                                                                                                                                                                                                                        Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Fig 5A-E; 90pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated DNA encoding sodium channel of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1998;
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                                                                                                          3567
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                                                                                                                                                                                   CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTTCCTGGAAAA 171
                                                                                                                                                                                                                 AAGGTTGTCGTCTACGCCCTGATCAGCGCCATACCTGCCATT-CTCAATGTCTTGCTGGT
                                                                                                                                                                                                                                            AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT
                                                                                                          TTTGGAAGGTGCATTAACGGGA 3588
                                                                                                                                   TTTGGGAAATGCATTCAATGGA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98FR-00014551.
                                        cDNA; 5875 BP
                                                                                                                                                                                                                                                                                   32.6%;
78.9%;
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                                                                                                                                                                                                                                                                                   Score 72.8;
Pred. No. 1
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1.1e-10;
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CTGCCTCATTTTCTGGCTCGTATTTTGTATCTTGGGAGTAAATTT--ATTTTCTGGGAAG

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                                                                                                            Query Match
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Matches 112
                                                                                                                                                                                                                                                                         This is the nucleotide sequence of an isolated nucleic acid which encodes the rat NAN channel (see AAY06596), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NAN channel cDNA was obtained from Sprague-Dawley rat DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse and human NAN nucleic acids (see AAX87600-02) and polypeptides (see AAX96596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NAN, methods for identifying agents that modulate NAN channel activity or NAN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NAN in sensory DRG and triceminal neurons provides a target for selectively
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                               sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The NaN gene has been named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1A-D; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat sodium channel NaN cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acids encoding sodium channels, used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY06596.
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20-NOV-1998;
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CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                               AAGGTTGTCGTCTACGCCCTGATCAGCGCCATACCTGCCATT-CTCAATGTCTTGCTGGT
                                                                    AAGGTGGTGAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT
                                                                                                                                                                               5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;
                                                                                                              Conservative
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98US-0109402P.
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/note= "these bases represent nucleotides missing from
the sequence given in Fig 1 of the specification. The
nucleotides are included to maintain the nucleotide
numbering given in the specification for this DNA
sequence"
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                                                                                                                              32.6%;
78.9%;
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                                                         CC The present sequence is that of cDNA encoding a novel rat tetrodotoxin CC resistant sodium channel, termed NaN (see AAB20122). The cDNA was CC isolated from a dorsal root ganglia tissue cDNA library by PCR CC amplification using generic primers (from conserved resions of a-subunit condium channel proteins) and NaN-specific primers (see also AAF30105-19), CC and RACE amplification. The open reading frame shows 73% similarity to CC the human NaN sequence (see AAF3010). NaN belongs to the a-subunit CC current. Such channels underlie the generation and propagation of current. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres. CC Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other current, makes it a very useful target for diagnostic and/or therapeutic cuses in relation to acute and/or chronic pain pathologies. A claimed current flow through NaN channels, or which modulates sodium current flow through NaN channels, or which modulates codium current flow through NaN channels, or which modulates codies associated with decreased sodium channel expression or considers associated with decreased sodium channel expression of considers associated with decreased sodium channel expression of considers associated with decreased sodium channel expression of disease, consider the recombinant production of NaN polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-103147/11.
P-PSDB; AAB20122, AAB20123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dib-Hajj S, Waxman SG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat sodium channel NaN cDNA.
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Query Match Best Local Similarity

32.6%; 78.9%;

Score 72.8; DB 4; Pred. No. 1.2e-10;

Length 5875;

Sequence

5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;

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                                                                                                                                                                                                                     Matches 112; Conservative
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Search completed: March 22, Job time: 165.414 secs 2004, 16:13:13 THIS PAGE BLANK (USPTO)

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Maximum Match 100%
Listing first 45 s
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match
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223
Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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15 US-10-388-470-1
12 US-10-288-470-1
12 US-09-804-0125-3
10 US-09-804-0125-3
10 US-09-804-0125-3
10 US-10-077-054-1
14 US-10-101-510-617
15 US-10-333-191-1
15 US-10-333-191-1
15 US-10-333-191-1
15 US-10-333-191-1
15 US-09-864-761-10437
1 US-09-864-761-110437
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Sequence 1, Appli
Sequence 1, Appli
Sequence 617, Appli
Sequence 617, Appli
Sequence 22921, A
Sequence 10437, A
Sequence 15573, A
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Sequence 366,
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Sequence 10175, A Sequence 1662, Ap Sequence 330, App	Sequence 2, Appli Sequence 1, Appli Sequence 238204,	Sequence 9, Appli Sequence 19, Appl Sequence 40, Appl Sequence 6181, Ap	e 3, 1 e 13, e 11, 1	17, 17, 15	e 5, e 60, e 63(	Sequence 61, Appl Sequence 13, Appl Sequence 14, Appl Sequence 1, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli

#### ALIGNMENTS

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Sequence 6, Application US/10388470

Publication No. US20030228662A1

GENERAL INFORMATION.

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Waxman, Stephen G.

FILE REFERENCE: 44574-5004-01-US

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/10/388,470

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/09/254,147C

PRIOR APPLICATION NUMBER: US/09/254,147C

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-01-29

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29
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US-10-388-470-6
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Best Local Similarity
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 44
                                                                                                         NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: Y = c or t.
OTHER INFORMATION: Leu.
                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 3701
48.3%;
96.0%;
  Score 107.8; DB 15; Pred. No. 2.8e-22;
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US-10-388-470-4
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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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                                                                                          Sequence 4, Application US/10388470 Publication No. US20030228662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143;
APPLICANT: Waxman, Stephen G. TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REFERENCE: 44574-5004-01-US CURRENT APPLICATION NUMBER: US/10/388,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
                                                          APPLICANT: Dib-Hajj, APPLICANT: Waxman, S
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NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 5860
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                                                                                                                                                                                                   SEQ ID NO 1
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                        FEATURE: NAME/KEY:
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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR PPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10388470 Publication No. US20030228662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G
                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (5804)
OTHER INFORMATION: cDNA sequence of mouse NaN,
                                                                      NAME/KEY: CDS
LOCATION: (41)..(53
OTHER INFORMATION:
                                                                                                                                                                  LENGTH: 5875
TYPE: DNA
ORGANISM: Rattus norvegicus
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LOCATION: (19)..(5313)
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ORGANISM: Mus musculus
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3448 AAGGTTGTTGTCAATGCCCTCATGAGTGCCATACCTGCCA-TCCTCAATGTCTTGCTGGT
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(1996)..(4042)
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                                                                            cDNA sequence
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82.5%;
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Pred. No. 7.8e-15;
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Best Local Similarity
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,693; 60/184,771; 60/184,131; 60/184,777; 60/184,773; 60/184,773; 60/184,773; 60/184,772; 60/184,772; 60/185,213; 60/185,216; 60/204,863; 60/204,815; 60/204,863; 60/204,815; 60/203,785; 60/204,821; 60/204,908; 60/204,825; 60/205,285; 60/205,232; 60/205,323; 60/205,324; 60/205,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
                                                                                                                                                 APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: n=a or c or g or t. Xaa at amino acid position INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn INFORMATION: or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 TTTGGGAAATGCATTCAATGGA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                             DAFFO, Abel
WRIGHT, Rachel J.
YAP, Pierre E.
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CHANG, Simon C.
CHEN, Alice
D'SA, Steven A.
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SPIRO, Peter A.
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                                                                                                                                                                                              HODGSON, David M.
LINCOLN, Stephen E.
                                                                                                                                                                                                                                   COHEN, Howard J.
                                                                                                                                                                                                                                                             YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
                                                                                                                                                                                                                                                                                                                                                                                  ROSEN, Bruce H. RUSSO, Frank D.
                                                                                                                                                                                                                                                                                                                                                                                                                   JONES, Anissa L.
LIU, Tommy F.
ROSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREENAWALT, Lila B.
HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DANIELS, Susan E.
DUFOUR, Gerard E.
                                                                                                                                                                                                                                                    CHEN,
                                                                                                                                                                                                                                                                                                                                                                   STOCKDREHER, Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREENAWALT
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Pred.
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No. 1
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1.5e-11;
nes 27;
                 ; 60/184,698;
; 60/184,776;
; 60/184,841;
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; 60/205,287;
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                                                                                                 60/184,770; 60/184,774
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; LOCATION: 6797, 7046, 7252, 7311, 7325-7326, 7502-7503, 7563
; OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-104
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                                                                                                                                                Query Match
Best Local Sim
Matches 106;
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Best Local Similarity bo...
107; Conservative
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. US20020061524A1
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SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6048)
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APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2323-155
CURRENT APPLICATION NUMBER: US/09/840,125
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,488
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte
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3949 TTTGAGGGCATGAGGGTGGTGGTCAATGCCCTGGTGGGCGCCATCCCGTCCA-TCATGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 TITGITTTCCATAAGGIGGIGGICAAIGCICCAAIAGGIGCCATACCICCAITCCIGAA
                                                40 TITGITTTCCATAAGGTGGTGGTCAAIGCTCTCATAGGTGCCATACCTCCCATTCCTGAA
                                                                                                                                                                                        Similarity
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68.6%; Pred. No. 1.7e-06;
tive 0; Mismatches 46
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                                                                                                                                                                                        Score 56; DB 9;
Pred. No. 1.9e-06;
                                                                                                                                                        Mismatches
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    4007
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US-10-077-054-1

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,994
FILING DATE: 02-Jul-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/514,907
FILING DATE: <Unknown>
ATTORNEY_AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
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APPLICANT: Ken Stokes

APPLICANT: Ken Stokes

Jos e Morissette

Jos e Morissette

TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC

TITLE OF INVENTION: SIGNAL SENSING BY CARDIAC PACEMAKERS THRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024Alris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4066
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MEDIUM TYPE: Floppy disk
                                                                                     4066
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4008 CGTCCTCCTCGTCTCATCTTCTGGCTCATCTTCAGCATCATGGGCGTGAACCTC-- 4065
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                                                                                                                                                                                                                                                                                                 40 TTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGCGGGAAGTTTGGGAGGTGCATCAACCAGA 4099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6048 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                          CGTCCTCCTCGTCTGCCTCATCTTCTGGCTCATCTTCAGCATCATGGGCGTGAACCTC--
                                                                                                                                                                                                                TGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCT 159
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                                                                                     TTTGCGGGGAAGTTTGGGAGGTGCATCAACCAGA 4099
                                                                                                                         TTTCCTGGAAAATTTGGGAAATGCATTCAATGGA 193
                                                                                                                                                                                                                                                        TTTGAGGGCATGAGGGTGGTCAATGCCCTGGTGGGCGCCATCCCGTCCA-TCATGAA 4007
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Pred. No. 1.9e-06;
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US-10-101-510-617
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                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION UNMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/077,054
CURRENT FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10077054 Publication No. US20030157600A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 617,
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(6054)
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (6774)
OTHER INFORMATION: a, t, c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Makielski, Jonathan C APPLICANT: Ye, Bin
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                    NAME/KEY: modified_base 
LOCATION: (7227)
                                                                                                                                                        LOCATION: (7021)
OTHER INFORMATION: a, t,
                                                                                                                                                                                         FEATURE: modified base
   NAME/KEY: modified_base
LOCATION: (7286)
OTHER INFORMATION: a, t,
                                                                           LOCATION: (7227)
OTHER INFORMATION: a, t,
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Pred. No. 1.9e-06;
       other or unknown
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RESULT 10
US-10-333-191-1
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                                                                                                                               ; NAME/KEY: misc_feature; LOCATION: (1)...(8491)
; OTHER INFORMATION: n may be any base US-10-333-191-1
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: Common Polymorphism in SC
TITLE OF INVENTION: Arrhythmia
FILE REFERENCE: 2323-154-II
CURRENT APPLICATION NUMBER: US/10/333,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR APPLICATION NUMBER: US 60/219;738
PRIOR APPLICATION NUMBER: US 60/219;738
PRIOR FILING DATE: 2000-07-20
NUMBER: DE STO. 150.000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10333191 Publication No. US20030235838A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTMARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 8491
                                                                 Matches | 106;
                                                                               Query Match
Best Local Similarity
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OTHER INFORMATION: a, t,
-10-101-510-617
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NAME/KEY: modified k
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NAME/KEY: modified base
LOCATION: (7477) ... (7478)
OTHER INFORMATION: a, t,
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NAME/KEY: modified_base
LOCATION: (7538)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (151)..(6198)
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo
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TTTGAGGGCATGAGGGTGGTGATGCCCTGGTGGGCGCCATCCCGTCCA-TCATGAA 4157
                               TTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAA 99
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                                                                 Conservative
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Pred. No. 2.2e
0; Mismatches
                                                                 <u>,</u>
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                                                               Score 56; DB 15;
Pred. No. 2.2e-06;
0; Mismatches 45
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PRIOR APPLICATION NUMBER: US

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US-09-864-761-22921/c
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
APPLICANT: Splawski, Igor
TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in Drug-induced Cardiac
TITLE OF INVENTION: Arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 8491
                                                                                                                                                                                                                                   Sequence 22921, Application US/09864761 Patent No. US20020048763A1
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Best Local (
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Publication No. US20030235838A1
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CURRENT APPLICATION NUMBER: US/10/333,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR FILING DATE: 2000-07-20
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LOCATION: (1)..(8491)
OTHER INFORMATION: n may be any base
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LOCATION: (151)..(6198)
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ORGANISM: Homo
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68.8%;
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Pred. No. 2.2e-06;
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APPLICATION NUMBER: US FILING DATE: 2000-05-2 FILING DATE: 2000-02-04

2000-05-26

60/207,456

US 09/632,366

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RESULT 13
US-09-864-761-10437
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; Patent No. US20020048763A1
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 20001-01-30
PRIOR PILING DATE: 20001-01-30
PRIOR PRILING DATE: 20001-01-30
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Best Local :
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ORGANISM: Homo
FEATURE:
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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FILLING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                             CCCCCAGGTGGTGGTGAACGCCCTCCTAGGCGCCATCCCCTCCA-TCATGAATGTGCTGC
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NN: EXPRESSED IN PLACENTA, SIGNAL = 3.3

NN: EXPRESSED IN HELA, SIGNAL = 4.9

NN: EXPRESSED IN HELA, SIGNAL = 3.9

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9

NN: EXPRESSED IN HEART, SIGNAL = 3.5

NN: EXPRESSED IN HEART, SIGNAL = 3.5

NN: EXPRESSED IN HEART, SIGNAL = 4.5

NN: EXPRESSED IN BRAIN, SIGNAL = 4.3

NN: EXPRESSED IN BONE MARROW, SIGNAL = 4.3

NN: SIGNAL = 3.9
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                            US/09864761
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Pred. No. 1.4e.
0; Mismatches
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO ACCIDENT.3
OTHER INFORMATION: EXPRESSED IN BRAIN
OTHER INFORMATION: EXPRESSED IN BONE
US-09-864-761-10437
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Best Local S
Matches 89
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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SOFTWARE: Annomax Sequence 1
SEQ ID NO 10437
LENGTH: 465
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COR APPLICATION NUMBER: PCT/US01/00662

COR FILING DATE: 2001-01-30

COR FILING DATE: 2001-01-30

COR APPLICATION NUMBER: PCT/US01/00661

COR APPLICATION NUMBER: PCT/US01/00670

COR APPLICATION NUMBER: US 60/234,687

COR FILING DATE: 2001-01-30

COR FILING DATE: 2000-09-21

COR FILING DATE: 2000-09-21
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OR PPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR APPLICATION NUMBER: PCT/US01/00664
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/774,203
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FILING DATE: 2001-01-30
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                                     AGTATACTTCCTT
                                                                                    TCCA-TCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTCAGCATCATGGG
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CGTAAATTTGTTT
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David K.
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IN BONE MARROW, SIGNAL =
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Pred. No. 9.3e-06;
0; Mismatches 43
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Sequence 15573, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.

David R. l, David K.

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OTHER INFORMATION: MAP TO ACC10127.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL
US-09-864-761-15573
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NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                        Local Similarity
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APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
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APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00670
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CCCATTCCTGAATGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGG 147
                                                                                                      TTTTCCTTTGCTTTTGCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCT 87
                                                                                                                                                  Conservative
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Pred. No. 9.5e-06;
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RESULT 15
US-09-919-039-366
Search completed: March 23, Job time: 152.581 secs
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN
FILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 6348
                                                                          3996 GTGTCTTATATTCTGGCTGATATTCAGCATCATGGGAGTAAATTTGTTT 4044
                                                                                                                                                3937 AGGGTCGTTGTGAATGCACTCATAGGAGCAATTCCTTCCA-TCATGAATGTGCTACTTGT 3995
                                                                                                112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTT 160
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                                                                                                                                                                                  52 AAGGTGGTGATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
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Listing first 45 summaries
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                            Pending Patents NA Main:*

1: /cgn2_6/ptcodata/2/pna/VSO16_COMB.seq:*
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6: /cgn2_6/ptcodata/2/pna/USO18_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES
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pna/US103A_COMB.seq:*
pna/US103B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 13. Application US/09646224A

GENERAL INFORMATION:

APPLICANT: Glaxo Mellcome PLC

APPLICANT: Tate, Simon N

APPLICANT: Tate, Simon N

APPLICANT: Hicks, Caroline A

TITLE OF INVENTION: Ion Channels

FILE REFERENCE: PG3432

CURRENT APPLICATION NUMBER: US/09/646,224A

CURRENT FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: GB 9805793.8

PRIOR FILING DATE: 1998-03-18

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 35

LENGTH: 223

C: TYPE: DNA
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77 US-60-213-846-1412
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10 US-10-388-470-1

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US-10-388-470-4
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US-10-144-771-19000
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Sequence 6, Appli
Sequence 6, Appli
Sequence 13985, A
Sequence 2171, Ap
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Sequence 310, Appli
Sequence 3, Appli
Sequence 1, Appli
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RESULT 3
US-60-207-214-72
; Sequence 72, Application US/60207214
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: USCLATED HUMAN T.
; TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-09-646-224A-13
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US-60-213-846-1109
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Best Local Simi
Matches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beasley, Ellen
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
CURRENT FILING NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID MOS: 1617
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1109
LENGTH: 3194
TYPE: DNA
ORGANISM: HUMAN
ORGANISM: HUMAN
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FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 CCCATCTGTTATGGTTTTCCTTTTGCTTTTCCATAAGGTGGTGGTCAATGCTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                    TAGGTGCCATACCTGCCATT
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               ISOLATED HUMAN TRANSPORTER PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF
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93.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 123.8; DB Pred. No. 8e-22;
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Pred. No. 3.1e-48;
; Mismatches 0;
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; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(115159)
; OTHER INFORMATION: n = A,T,C or
US-60-466-412-84151
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; ORGANISM: HUMAN
US-60-207-214-72
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FBBLSEQ for Windows Version 4.0
SEQ ID NO 84151
LENGTH: 115159
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LENGTH: 6925
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CURRENT FILING DATE: 2000-5-26
NUMBER OF SEQ ID NOS: 622
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                 84408 TAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTA
                                                                                                                                                                                                                  84350 CCCATCTGTTATGGTTTTC--TTTGCTTTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCA 84407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2738 CCCATCTGTTATGGTTTTC--TTTGCTTTTGTTTCCATAAGGTGGTGGTCAATGCTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
                                                                                                                                                         74 TAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                            CCCATCTGTTATGGTTTTCCTTTGCTTTTGTTTTTCCATAAGGTGGTGGTCAATGCTCTCA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
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                                                                      TTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAATTTGGGAAAATGCATTCAATGGA 193
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        ACAGACT 200
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                                                                                                                                                                                                                                                                                                     Conservative
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93.0%;
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93.0%;
                                                                                                                                                                                                                                                                                                 Score 123.8; DB 103; Length 115159; Pred. No. 2.1e-21; 0; Mismatches 7; Indels 6; Ga
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Pred. No. 9.9e-22;
0; Mismatches 7
                                                  -TTTTCTGGAAAATTTGGGAAATGCATT-AATGGA 8452
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RESULT 6
US-60-213-846-1412
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                                                                                                                                                                                                                                                                 APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
CURRENT APPLICATION NUMBER: US/60/213,846
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID MOS: 1617
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1412
LENGTH: 3163
TYPE: DNA
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1412, Application US/60213846 GENERAL INFORMATION:
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                                                                                                                                                          Matches 143;
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Best Local S
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CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 60/666,225
EARLIER FILING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.0
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TITLE OF INVENTION: A Voltage-Gated Nervous Tissue Sodium Channel,
TITLE OF INVENTION: Polynucleotides Encoding Therefor, and Methods of Use
TITLE OF INVENTION: Thereof
FILE REFERENCE: R0021B-REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Khare, Reena
APPLICANT: Rabert, Douglas K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fish, Linda M.
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                                                                                                                                                                                 Local Similarity
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Local Similarity 96.0%;
                                                                        2330 AAGGTGGTCAATGCTCTCATAGGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGT 2388
112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
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                                                                                                      52 AAGGTGGTCGATAGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AAGGTGGTCGATAGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
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                                                                                                                                                            Conservative
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                                                                                                                                                          Score 107.8; DB 77; Length 3163; Pred. No. 1.3e-17; 0; Mismatches 2; Indels 4;
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2389 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA 2446

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RESULT 7
PCT-US00-19342-6
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                                           SOFINGTH: 3701
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application PC/TUS9902008D GENERAL INFORMATION:
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                                                                                   TITLE OF INVENTION: Dorsal Root Ganglia-Specific and Tetrodotoxin Resistant TITLE OF INVENTION: Voltage-Gated Sodium Channel, S. Dib-Hajj et al. FILE REFERENCE: 44574-5004-WO, Yale University CURRENT APPLICATION NUMBER: PCT/US99/02008D CURRENT FILING DATE: 1999-01-29 EARLIER APPLICATION NUMBER: US 60/072,990 EARLIER APPLICATION NUMBER: US 60/072,990 EARLIER FILING DATE: 1998-01-29 EARLIER FILING DATE: 1998-01-29 EARLIER FILING DATE: 1998-01-29 EARLIER FILING DATE: 1998-01-29 EARLIER FILING DATE: 1998-01-20 NUMBER: US 60/109,402 EARLIER FILING DATE: 1998-01-20 NUMBER OF SEQ ID NOS: 40 SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/354,147
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APPLICANT: Waxman, Scephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-02-WO
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LOCATION: (1)..(3699)
OTHER INFORMATION: partial human
                            TYPE: DNA
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ORGANISM: Homo sapiens
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nes 143; Conserv
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ilarity 96.0%;
Conservative
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Pred. No. 1.4e.
0; Mismatches
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APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
FITLE OF INVENTION: Modulation of Sodium Channels in Dor
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,990
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
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US-10-388-470-6
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GENERAL INFORMATION:
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Best Local Similarity
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NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: Y
OTHER INFORMATION: L
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LOCATION: (1)..(3699)
OTHER INFORMATION: pa
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                                    112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
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Pred. No. 1.4e-17;
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Pred. No. 1.4
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                                                                                                                                                                                    Length 3701;
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   -TTTTCTGGAAAA 3012
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RESULT 10
US-10-170-235-13985
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; ORGANISM: HUMAN
US-10-170-235-13985
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US-60-453-050-2171
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN

TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE REFERENCE: CL001380

CURRENT APPLICATION NUMBER: US/10/170,235

CURRENT FILING DATE: 2003-03-17

NUMBER OF SEQ ID NOS: 42514

SEQ ID NO 13985

LENGTH: 5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2171, Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                       Query Match 48.3%;
Best Local Similarity 96.0%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                      PILE REPERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FRACESEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
TYPE: DNA
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Local Similarity 96.0%;
hes 143; Conservative
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TTTGGGAAATGCATTCAATGGAACAGACT 200
                                                CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA 3763
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                                                                                                                                                                                                                       Score 107.8; DB 102; Length 5080; Pred. No. 1.5e-17; 0; Mismatches 2; Indels 4;
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Pred. No. 1.5e-17;
0; Mismatches 2
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Sequence 2171, Application US/60466412
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND
FILE REFERENCE: CLO01466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
TYPE: DNA
ORGANISM: Homo sapiens
US-60-466-412-2171
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US-60-466-412-2171
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-2171
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2171, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF FILE REPERENCE: CLOO1456
                                                                                                                                                                                                                         Match 48.3%;
Local Similarity 96.0%;
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Local Similarity 96.0%;
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                                                                        CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA
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        TTTGGGAAATGCATTCAATGGAACAGACT 200
                                              CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTC--TTTTCTGGAAAA
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Pred. No. 1.5e-17;
0; Mismatches 2
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Pred. No. 1.5e-17;
0; Mismatches 2
                                                                                                                                                                                                                                                 DB 103; Length 5080;
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3764

TTTGGGAAATGCATT-AATGGAACAGACT 3791

RESULT 14 US-10-219-051B-910

Sequence 910, Application US/10219051B GENERAL INFORMATION: APPLICANT: The General Hospital Corporation doing business as Massachusetts General APPLICANT: Hospital / Bayer AG

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SOUTWARE: Perl script
SEQ ID NO 910
LENGTH: 5728
TYPE: DNA
ORGANISM: Homo sapiens
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US-10-296-130-3
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                                                                                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 3
LENGTH: 5728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10296130 GENERAL INFORMATION:
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Best Local Similarity 96.0%;
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                                                                                                                                                                                                                                                         APPLICANT: KANAZAWA, Ichiro
APPLICANT: KANAZAWA, Ichiro
APPLICANT: GOTO, Jun
APPLICANT: JEONG, Seon-Yong
TITLE OF INVENTION: Human Sodium Channel SCN12A and SCN8A
FILE REFERENCE: 2002-1512A/WMC/00653
FULL REFERENCE: 2002-1512A/WMC/00653
CURRENT APPLICATION NUMBER: US/10/296,130
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: PCT/JP00/04629
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)..(5728)
OTHER INFORMATION: n=a, c, g or t
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: EMBL / AF150882
DATABASE ENTRY DATE: 2000-01-16
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP2000-152085
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 18
NAME/KEY:
LOCATION:
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                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                              EATURE:
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CDS
(200)..(4534)
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Pred. No. 1.5e-
0; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified base LOCATION: 5632
OTHER INFORMATION: n = a, g, c or t
PUBLICATION INFORMATION: AUTHORS: Soen-Yong Jeong et al.
TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel a Subunit TITLE: Gene, SCN12A
                                                                                                                                                                                                                                                                                                                                                             ISSUE: 1
PAGES: 262-270
DATE: 2000-01-15
DATABASE ACCESSION NUMBER: GenBank AF150882
DATABASE ENTRY DATE: 2000-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL: Bic
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                                      172 TTTGGGAAATGCATTCAATGGAACAGACT 200
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TTTGGGAAATGCATT-AATGGAACAGACT 3836
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                                                                                     TTTTCTGGAAAA 3808
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Search completed: March 23, 2004, 04:00:18 Job time: 1684.54 secs

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Sequence:
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Maximum DB
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Maximum Match 100%
Listing first 45 s
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seq length: 2000000000
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25.1 4852

25.1 4855

24.9 4855

24.9 4855

24.4 201

22.6 5874

22.6 5874

22.5 6524

600

19.8 600

19.8 32100

15.8 32100

15.8 32100

15.8 32100

14.3 165502

14.3 165502

14.3 234309

14.3 234309

14.3 234309

14.3 1790242

14.3 1790242

14.2 1413

14.2 37544

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Match
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223
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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US-60-548-091-5675
US-60-548-091-267
US-60-548-091-268
US-60-548-091-268
US-60-548-091-523
US-60-548-091-5578
US-60-548-091-5578
US-60-548-091-5578
US-10-487-337-5
US-60-545-213-3189
US-60-545-213-3189
US-10-765-790-73
US-10-767-471-10601
US-10-796-280-12318
US-10-796-380-12318
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Sequence 5675, Apsequence 267, App Sequence 268, App Sequence 5534, Ap Sequence 5523, Ap Sequence 5578, Appli Sequence 578, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1349, Ap Sequence 13405, Ap Sequence 10601, A Sequence 10601, A Sequence 12378, A Sequence 12378, A Sequence 12378, A Sequence 10805, App Sequence 3471, App Sequence 3471, App Sequence 392, App Sequence 5044, App Sequence 5044, App Sequence 5044, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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RESULT 2
US-60-548-091-267
; Sequence 267, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001506
; CURRENT APPLICATION UNMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc\_feature
LOCATION: (1)...(100374)
OTHER INFORMATION: n = A,T,C

or G,

or insertion/deletion polymorphism (see Tables

LENGTH: 100374 TYPE: DNA

31.2 14.0 1790242 6 US-10-767-471-10805 31 13.9 185248 6 US-10-767-95-6395 31 13.9 185248 6 US-10-796-280-13228 30.8 13.8 30.0 6 US-10-779-543-1428 30.8 13.8 681 6 US-10-779-543-1428 30.8 13.8 681 6 US-10-779-543-4539 30.8 13.8 876 6 US-10-779-543-4539 30.8 13.8 131646 7 US-60-550-051-3063 30.8 13.8 303523 6 US-10-796-280-12202 30.8 13.8 645179 6 US-10-796-280-12317 30.6 13.7 99100 1 PCT-US03-35879-1 30.6 13.7 99100 1 PCT-US03-35879-1 30.4 13.6 1049 6 US-10-796-280-12462 30.4 13.6 1049 6 US-10-796-280-12462 30.4 13.6 22372 6 US-10-796-280-12462 30.4 13.6 22372 6 US-10-796-280-12462 30.4 13.6 65558 6 US-10-796-280-12462 30.4 13.6 65558 6 US-10-765-790-103 AL INFORMATION: CARGILL, Michele et al. E OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED B OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED E OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED E OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED E OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED ENT FILING DATE: 2004-02-27 ER OF SEQ ID NOS: 24433 WARE: FastSEQ for Wildows Version 4.0	RESULT US-60-5 Seque GENER GENER FITL TITL FILE CURR CURR NUMB		42.4		<b>.</b> .	4 4 3 1	40	ω	w	α ω	w	LJ I	w	C 33	ω	w	w	23	28	0 2																		
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Best Local Simi
Matches 102;
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                                                                                         TGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGA 168
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                  AAATTTGGGAAATGCATTCAATGGA 193
                                                                                                                                                            CATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCT 108
AAGTTTGGGAGGTGCATCAACCAGA 82101
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; ORGANISM: Homo sapiens
US-60-548-091-267
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FOSTSEQ for Windows Version 4.0
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 267
LENGTH: 4852
Sequence 268, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
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Best Local Similarity 63.2
Matches 115; Conservative
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Pred. No. 2.8e-07;
0; Mismatches 45
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Pred. No. 2.8e-07;
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SOFTWARE: FastSEQ ID NOS: 24433

SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 268
LENGTH: 4855
TYPE: DNA
ORGANISM: Homo sapiens
US-60-548-091-268
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001506
FILE REFERENCE: CL001506
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5534
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USE:
FILE REFERENCE: CL001506
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Pred. No. 3.6e-07;
1; Mismatches 45
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APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
APPLICANT: LOUIS BOON
APPLICANT: John Nicholas WOOD
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND
FILE REFERENCE: 117-492 / N. 86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT APPLICATION NUMBER: PCT/GB02/03852
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR PILLING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
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Best Local Similarity
Thes 79; Conserve
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; ORGANISM: Homo sapiens
US-60-548-091-19210
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; ORGANISM: Homo sapiens
US-60-548-091-5523
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 19210
LENGTH: 201
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CURRENT | APPLICATION NUMBER: US/60/548,091

CURRENT | FILLING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTWARE: FRANCEQ for Windows Version 4.0

SEQ ID NO 5523

LENGTH: 201
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Best Local Similarity 72.3%;
                                                                 NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 CGTCCTCCTCGTCTGCCTCATCTTCTGGCTCATCTTCAGCATCATGGGCGT 201
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                                              5874
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71.2%;
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Pred. No. 4e-06;
1; Mismatches 30;
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Pred. No. 6.6e-07;
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APPLICANT: LOUIS POON
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REFERENCE: 117-492 / N. 86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5578
LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001506
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NAME/KEY: CDS
LOCATION: (1)..(587.
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
                                                                                                                                                                                                                                                APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 TGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTT 156
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Pred. No. 1.4e-05;
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Pred. No. 5.2e-06;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (204)..(6074)
; OTHER INFORMATION:
US-10-487-337-1
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LENGTH: 600
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Best Local Similarity
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                                                                                                                                                          Sequence 8171, Application US/60545213
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
SOFTWARE: PatentIn version SEQ ID NO 8171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
                                 APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Rattus norvegicus
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Pred. No. 0.00047;
0; Mismatches 33;
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Pred. No. 1.
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                                                               Sequence 13405, Application US/10100683
GENERAL INFORMATION:
APPLICANT; Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
CURRENT FILING DATE: 2002-03-19
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
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TYPE: DNA
ORGANISM: Homo sapiens
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Similarity 68.8%;
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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Pred. No. 0.00047;
0; Mismatches 33
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APPLICATION NUMBER: US 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: US 60/056,845

FILING DATE: 1997-08-22

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US-60-548-091-5539

US-60-548-091-5539

Sequence 5539, Application US/60548091

GENERAL INFORMATION:

APPLICANT: CARCILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001506

CURRENT APPLICATION NUMBER: US/60/548,091

CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 5539

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13405
LENGTH: 32100
TYPE: DNA
ORGANISM: Homo sapiens
S-10-100-683-13405
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APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
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APPLICATION NUMBER: US 60/043,314
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GGTGGGCGCCATCCCGTCCA-TCATGAACGTCCTCCTCCTCGTCTGCCTCATCT 201
                                       CATAGGTGCCATACCTCCATTCCTGAATGTTTTGCTTGTCTGCCTCATTT 122
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1 (bases 1 to 4614)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, C. Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
                2 (bases 1 to 4614)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Podd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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    Direct Submission
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VIRTUAL TRANSCRIPT, partial sequence,
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CE534807 768167 MA
BU116614 603139753
CE190928 tigr-988-
AY416499 Homo sapi
BG548184 602575340
CD348085 UI-M-FY0-
BU117962 603143496
CB457889 716006 MA
A1259694 Tetraodon
ZC5172038 tigr-988-
CE574768 tigr-988-
CE35411 tigr-988-
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1 (bases 1 to 496)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.S., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au moder,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au moder,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au modern and the state of the state
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping scanning the human genome proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-2003) Celera Genomics,
                                                                                                                                                                                                                                                BAC end Web Server: http://www.htsc.washington.
Plate: 2119 row: N column: 5
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                            Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AQ605323.1 GI:5065317
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Location/Qualifiers
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                                        /mol_type="genomic DN
/db_xref="taxon:9606"
                                                                  organism="Homo sapiens"
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/locus_tag="HCM1903"
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Best Local
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                                                                                                                       al Similarity
132; Conserv
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                                                                                      52
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                     Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                       This sequence was made by sequencing them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 302 (5652), 1960-1963 (2003)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14671302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGTGCCATACCTGCCATT-CTGAATGTTTTGCTTGTCTGCCTCATAATCTGGCTCGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTGTATTCTGGGAGTATACTTCCTTT 161
CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                       AAGGTTGTTGTCAATGCCCTCATGAGTGCCATACCTGCCA-TCCTCAATGTCTTGCTGGT
                                                                          AAGGIGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 4556)
                                                                                                                       37.5%;
nilarity 82.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                    'gene="SCN11A"
'locus_tag="HCM1903"
                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                       organism="Mus musculus'
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88.5%;
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Pred. No. 1e-1
0; Mismatches
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                                                                                                                       Score 83.6; DB 29;
Pred. No. 3.5e-09;
0; Mismatches 24;
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VIRTUAL
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                                                                                                                                                         4556;
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                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JAN-2003) The Sanger Institute, (Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 800)
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BX238165
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 616)
                                                                                                                                                                          AZ623890
AZ623890.1 GI:11746080
GSS.
                                                                                                                                                                                                                                 1M0462J06F Mouse 10kb plasmid clone UUGC1M0462J06 F, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humphray, S.J., Huckle, E. and Durham, J.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio
                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                          AZ623890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was generated from the SP6 end of BAC 286P24. 286P24 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX238165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAATGTGTTGCTGGTGTGCTTGATCTTCTGGCTGATCTTCAGCATCATGGGGGGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTTTTCCTGGAAAATT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGCGTTTCTGTTTTTGTAGGTGGTAGTGAACGCTCTTCTTGGAGCCATACCTTCCA-TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCTTTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="DKEY-286P24"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Danio rerio"
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69.1%;
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Pred. No. 0.0011;
                                                                                                                                                                                                                                   genomic survey sequence.
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DKEY-286P24,
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d UUGC1M library Mus
                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 29;
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thi; Muridae; Murinae; Mus
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  Z86508.1 GI:1883420
GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0462 row: J column: 06
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                               F.rubripes
Z86508
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Location/Qualifiers
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                                                                                                                     FR0002725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                        TTTGCTTTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATT 93
                                                                                                                                                                                                                 CCTCTTCGCCGGGAAATTTTCGAGATGTGTCGACACCAGAAGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 bp mRNA linear EST 27-AUG-1 ot73e07.81 Soares_total_fetus_Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1622436 3' similar to 9b:M81758 SODIUM CHANNEL PROTEIN, SKELETAL MUSCLE ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
AI016157
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1 (bases 1 to 407)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V_type: phage PRIMER: M13
                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1636 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 472) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                Unpublished (1997)
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 404.
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/mol type="genomic DNA"
/db xref="taxon:31033"
/clone="010M03aB3"
                                                              /organism="Homo sapiens"
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clone="IMAGE:1622436"
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                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Actinopterygii; Neopterygii; Percomorpha; Tetradontoidea; Takifugu.

E 1 (bases 1 to 619)
8S Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.

Bijar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.

Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: ml3mp18
V_type: phage
PRIMER: M13
     113
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Takifugu rubripes
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 TGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAAT 172
                                             Addrigetrerenancecrerearedeckircecreck-rearedakeerecreere
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/mol_type="genomic_DNA"
/db_xref="taxon:31033"
/clone="010M03aE3"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                   clone_lib="cosmid 010M03"
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                                                                                                                        Score 52.6; DB 29;
Pred. No. 0.048;
0; Mismatches 39;
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                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
cross match v0.990329.
Seq primer: AGCGGATAACAATTTCACACAGGA.
                                                         CA358980 763 bj 631834 NCCCWA 1RT Oncorhynchus mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                        85;
Oncorhynchus mykiss (rainbow trout)
                            CA358980
CA358980.1
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11876 Leetown Road, Kearneysville, 1
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Rexroad, C.E. and Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence analysis of a rainbow trout normalized cDNA library
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/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2:
Library made from pooled tissue from brain, gill,
spleen, muscle, and kidney."
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/clone="1RT29H17_B_D09"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Oncorhynchus mykiss"
|mol_type="mRNA"
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                              GI:24604167
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Pred. No. 0.052;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                         Tetraodon : 030G19 of
                Nat. Gen.
20296633
                           Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                             GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                      Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C. Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
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/clone="1RT5D21 B B11"
/tissue_type="pooled"
/lab_host="DH10B"
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library B from Tetraodon
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nigroviridis,

DNA

linear

r GSS 01-SEP-2000 end of clone genomic survey

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158 ATGTGTTGCTGGTTTGCCTCATCTTTTGGCTGATTTTCAGTATCATGGGAGTCAACTTGT 217
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 763)
Rexroad, C.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: crexroad@ncccwa.are.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified t
cross_match v0.990329.
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                                                ATGITTTGCTTGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCC 158
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                                                                                                                                                                                            TTTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGA 98
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NCCCWA 1RT"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2:
Library made from pooled tissue from brain, gill,
spleen, muscle, and kidney."
                                                                                                                                                                                                                                                               Score 52.4; DB 14;
Pred. No. 0.051;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome o freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                        1 (bases 1 to 751)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                             BU226444 751 bp mRNA linear EST 26-NOV-2002 603946353F1 CSEQCHN23 Gallus gallus cDNA clone ChEST899j14 5', mRNA
                                                      Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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PO Box 88, Manchester, M60 1QD, Tel: 01612008930
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/mol_type="genomic DNA"
/db xref="taxon:99883"
/clone="030G19"
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Pred. No. 0.062;
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                                                          of Science and Technology
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CB608527.1
EST.
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AMGNNUC:NRDG1-00143-D3-A nrdg1 (10855)
nrdg1-00143-d3 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                       Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                             Tel: 805 447-4881
Plate: 00143 row: d column:
                                                                                                                                                                                                                                                 One Amgen Center Drive, Thousand Oaks,
                                                                                                                                                                                                                                                                                                                                               Amgen
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                       Amgen,
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                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="CSEQCHN23"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
              /mol_type="mRNA"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="ndg1-00143-d3"
/tissue_type="Dorsal Root Ganglia"
/clone_Tib="nrdg1 (10855)"
/note="Vector: pSPRT1; Site_1: Sal1; Site_2: Not1;
dorsal root ganglia"
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                                                                                                                                                                                                                                                                                                                                             Program.
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                                                                                                                                                  organism="Rattus norvegicus"
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72.5%;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
cross_match v0.990329.
plate: LAM8018 row: M column: 21
Seq primer: TAGAAGGCACAGTCGAGG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB534807 519 bp mRNA linear 768167 MARC 6BOV Bos taurus cDNA 3', mRNA sequence. CB534807 CB534807.1 GI:29400892 EST.
Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
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                                      TGTGCTGCTTGTCTCATCTTCTGGCTGATCTTTAGCATTATGGGTGTGAATTTGTT
                                                              TGTTTTGCTTGTCTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCT
                                                                                                               TTTGAAGGCATGAGGGTCGTTGTGAATGCTCTTGTTGGAGCAATTCCCTTCCA-TCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCAGCATCATGGGCGTGAACCTCTTCGCCGGGAAATTTTCG 182
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                                                                                                                                                 TTTGTTTTCCATAAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAA
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                      /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: Not Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."
                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Bos taurus"
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Pred. No. 0.17;
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                                                                                                                                                     112 CTGCCTCATTTTCTGGCTCGTATTTTGTATTCTGGGAGTATACTTCCTTTTCCTGGAAAA 171
                                                                                                                                                                                           406 AGGGTGGTTGTCAATGCCTTGGTTGGCGCTATCCCTTCTATT-ATGAATGTCTTGTTGGT
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                                                                                                                                                                                                                                52 AAGGTGGTGGTCAATGCTCTCATAGGTGCCATACCTCCCATTCCTGAATGTTTTGCTTGT 111
                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 833)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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BU116614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO Box 88, Manchester, M60 1QD, UK
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/note="organ: brain; Vector: pBluescript II KS(+); Site_1: RcoRI; Site_2: Not1; Modification of pBluescript II KS(+); Etratagene] vector to accommodate cDNA produced with the "-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcRI. Ligate in double stranded adaptor containing BsgI and BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaag] [5'aattctttttttcggatccggggctgcacgc]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Compton Line 151"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Female"
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Search completed: March 22, 2004, 23:12:48 Job time : 1321.4 Becs

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX017230	RESULT 1
Mammalian sodium channel proteins Patent: WO 9947670-A 14 23-SEP-1999;	Tate, S.N., Grose, D.T. and Hick, C.A.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)	•	AX017230.1 GI:10042150	AX017230	Sequence 14 from Patent WO9947670.	AX017230 244 bp DNA linear PAT 07-SEP-2000		

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RESULT 2
BD138452
LOCUS
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OS Homo sapiens
PN JP 20025089-
PD 26-MAR-2002
PF 18-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 244)
Grose, D.T., Hick, C.A. and Tate, S.N.
Mammalian sodium channel protein
Patent: JP 2002508941-A 13 26-MAR-20
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                                                                                                                                                                                                                                    PR 18-MAR-1998 GB 9805793.8
PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE
C1215/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JP 2002508941-A/13
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18-MAR-1999 JP 2000536853
18-MAR-1998 GB 9805793
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JP 2002508941-A 13 26-MAR-2002;
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K CAROLINE ANNE (GB)
Location/Qualifiers
                                                                          /organism='Homo sapiens (human)'.
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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             /mol_type="genomic DN
/db_xref="taxon:9606"
                                            organism="Homo sapiens"
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Pred. No. 4.5e-69;
); Mismatches 0;
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DEFINITION
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                                                                                                                                 Direct Submission

Direct Submission

Submitted (07-OCT-2003) Genome Center, University of Wasnı
Submitted (07-OCT-2003) Genome Center, University of Wasnı
Sox 352145, Seattle, WA 98195, USA
On Oct 7, 2003 this sequence version replaced gi:21622736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167476 bp
Homo sapiens chromosome 3 clone
AC116038
AC116038.3 GI:37537604
                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 167476)

Kaul,R.K., Olson,M.V., Raymond,C. and Hauger
Direct Submission
Submitted (23-MAR-2002) Genome Center, Unive
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 167476)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenthimmachak,C., Phelps,K.A., Buckley,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                       Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 167476)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (28-JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 167476)
                                                                                                                                                                                                                                                                                                                                  and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Pred. No. 4.5e-69;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      Center,
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Haugen, E.D
                                                                                                                                                                                                University of Washington
                                                                                                                                                                                                                                                                                                    University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                          University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rouse, G., Wu, Z., Raymond, C. and
                                                                                                                                                                                                                                                                                                                                               Rouse, G., Wu, Z.,
Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                           Rouse, G., Wu, Z. Raymond, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          of Washington,
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	3468 3447 179 <800 2649 2744	727 745	6640 6560 4721 4667 2738 2744	<800 3014 3028 8136	4167 999 990 2583	<800 1364 1346 4036 4036	7486 7486 7486 7486 7486 7486 7486 7486		3447 184 6800 1923	4771 4809 4878 2537	2016 2003 2707 2741 2813 2744	9345 9792 449 <800 2317 2259	2248 2299 512 <800 5097 5007	6 <800 6382 6514 2067 2008	8696 8629 2732 2741 2234 2259	SeqDerMap FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	HindIII	between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.	int and hence do not applicant remaining discrep	vector, in order to accurately represent the entire circular BAC.  Small fragments below a variable cutoff (approximately 400-800 bp)	fragments with sequence-predicted fragments is given below.  The electronically-digested sequence consists of both insert and	This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest	Sequence Validation:		quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were	all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred	This sequence was finished as follows unless otherwise noted:	not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	l error in 10,000 bp. Base-by-base quality values are	estimates computed by the Phrap assembly program.	Sequence Quality Assessment: This entry has been annotated with semience muality	5': RP11-1114A3 AC13/625, 2001-DD OVERTAD 3': RP11-182A24 (UWGC:bc0782) AC123903, 41341-bD overlap	Overlapping Sequences:	Quality coverage: 18.9x in Q20 bases; sum-of-contigs	Consensus quality: 167476 bases at least Q30 Consensus quality: 167476 bases at least Q20	least	Chemistry: Dye-terminator Big Dye; 55% of reads
	1 1 1 1	731	1568	835	309	1565	8662	560 .	9961	3711	3737	57	1 1 0 0 0	500	6166	7181	651	2264	8729	19834	2709	2583	775	1620	182	1368	712	2038	2328	331	8963	6613	5080	553	762	3049	687
6843		1501	1560 602 <8	822 511 <8	<800 7414 75	1560 1229 11	8629 3569 36	<800 4463 44	9792 1341 13	3718 324 <8	1975	4023	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1172	3594	7213 166 <8	<800 391 <8		01	19753 475 <8	2686 5528 53		<800 438 <8		<800 5444 53		μ,	2003 1053 10		<800 240 <8	9211 5478 53			<800 8072 81	<800 1891 18		<800 7123 71
6824 3630 3/2/	:		<800 1242	<800 253	7557 3335	1188 2731	3639 6314	4430 344	1346 1967	<800 1198	:	:		1188 4240		<800 2486	<800 4714	5089 396		<800 790 ·	5397 3725	1408 2044	<800 1294	1228 4079	5397 3022	<800 694	3264 1222	1068 178	4878 4728	;	5397 5748	. ,	<800 3588	8171 4636	1888 6949	2040 5020	7158 2550 2550

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ACCESSION
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KEYWORDS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anquiano, D., Anyabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Censer, M., Center, A., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Davila, M.I., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Franeer, C., M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hollins, B., Howells, S., Hulayk, S., Hune, J., Idebird, D., Jackson, A., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Koyas, C., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kett, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCGTTTATGCAGCTGTTGATTCCACAGAGGTGAGTCAGTGTTTCTACCATGTTCGGCAGT 120
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Pred. No. 4.4e-63;
0; Mismatches 11
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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, Z., Meenen, E., Mahingy, S., McGodd, M.P., McKeill, T.Z., Meenen, E., Milosavjavic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavjavic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavjavic, A., Miner, G., Minja, E., Montemayor, J., More, S., Parks, K., Morgan, M., Morris, K., Morris, S., Minidasa, M., Murphy, M., Nair, L., Nankervia, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pallyse, F., Policker, K., Morris, S., Parks, K., Parks,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GXXU
Center clone name: CH230-51503
Center clone name: CH230-51503
Consensus quality: 177120 bases at least Q40
Consensus quality: 179072 bases at least Q30
Consensus quality: 180314 bases at least Q30

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft\_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is

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SOURCE
ORGANISM
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Best Local :
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                                                                                              AUTHORS
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                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., A
fallen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
lanyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Be
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                          AC127215.4 GI:24940804
                                                                                                                                                                                                                                                                             unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                              GTGCTATGAATGTGTGGACGGCCC 85860
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATCATGACTACATGGACAGTCC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTCCAGAGAGGTGAGTTAATGTCTCACTGTGTTCTAGAATGTCATGCTCAAACCGGAG 85836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTCCACAGAGGTGAGTCAGTGTTCTACCATGTTCGGCAGTGTTATGGTCAAGTCAGAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 243048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208133
208233
209539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                norvegicus clone CH230-10N16, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="wgs_end_extension clone_end:Sp6" 206411 . 208132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202141. .203014
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cione_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202181. .202273
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203916. .205212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130181. .131269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-51503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="wgs_end_extension:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .210800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208132: contig of 208132 bp in length 208232: gap of unknown length 209538: contig of 1306 bp in length 209638: gap of unknown length 209638: gap of 1162 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence:RXBVQ86TJB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence: BZ189873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76.8; DB 2;
Pred. No. 9.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                    Barnstead, M., Benahmed, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 210800;
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                                                                                          Adams, C., Alder, J.,
                     Brown, M.,
                                                                                                                                                                                                                                                                                                                    HTG 13-NOV-2002
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Chardenas W., Coartes, K., Coavaros J., Coesar, H., Center A., Chocke, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockreal, R., Cox, C., COyle, M., Cree, A., D. Scuard, L., Davis, G., Davy, Garroll, L., De, Anda, C., Dederich, D., Delgado, O., Denson, S., Davy, Garroll, L., De, Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Beachto, M., Dubain, R., Dubain, K., Duval, B., Eaves, K., Egan, A., Beachto, M., Bugene, C., Brans, C.A., Fells, T., Fan, G., Prernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Gostra, M., Guerra, M., Marin, J., Martin, S., Munidasa, M., Muniphy, M., Rait, L., Martin, J., Martin, G., Muniphy, M., Rait, L., Martin, J., Martin, G., Muniphy, M., Rait, L., Martin, J., Martin, G., Muniphy, M., Rait, L., Martin, J., M
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Center: Baylor College of Medicine Center code: BCM

JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

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RESULT 6
AC124662
                                           REFERENCE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                             EYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                       29458 GTGCTATGAATGTGTGGACGGCCC 29435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                         AC124662
Mus musculus chro
IN PROGRESS ***,
1 (bases 1 to 241289)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 9, clone RP24-409K22
                                                                                                                                                                                  AC124662
AC124662.5
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                 Mus musculus
                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATTCCACAGAGGTGAGTCAGTGTTCTACCATGTTCGGCAGTGTTATGGTCAAGTCAGAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                ATATCATGACTACATGGACAGTCC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTCCAGAGAGGTGAGTTAATGTCTCACTGTGTTCTAGAATGTCATGCTCAAACCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                                                                                                                                                                                                                         musculus chromosome 9 clone RP24-409K22 map 9, PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241920
242020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 229285 bases at least Q40 Consensus quality: 231657 bases at least Q30 Consensus quality: 231185 bases at least Q20 Estimated insert size: 236807; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: CH230-10N16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- Summary Statistics
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: GDUK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="clone_boundary clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_contig"
240939. .241455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end_sequence:BH308290"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="CH230-10N16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
                                                                                                                                                                                  GI:38490569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .243048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1_type="genomic DNA"
_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241919: contig of 241919 bp in length 242019: gap of unknown length 243048: contig of 1029 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 76.8; DB 2;
Pred. No. 9.2e-14;
                                                                                                                                                                                                                                                                       241289 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 243048;
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                                                                                                                                                                                                                                                                       HTG 22-NOV-2003
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                                                                                                                                                                                                                                                   SEQUENCING
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REFERENCE
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3 (bases 1 to 241289)

8 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Birren, B., Nusbaum, C., Lander, B., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Choepel, Y., Colymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Faro, S., PitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hifez, N., Halez, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Tiliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacCean, C., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacCean, C., MacCarthy, M., MacConald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., MacConald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., MacConald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Iver, J., Peterson, K., Phunkhang, P., Pierre, N., O'Neil, D., Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Yassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-NOV-2003) wnitering and 2141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 22, 2003 this sequence version replaced gi:38153914. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Thodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Nature, C., Talamas, C., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                        as soon as it is available and the accession number will be preserved.
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Center clone name: 409_K_22
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Center: Whitehead Institute/ MIT Center for Genome Research
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Buffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Maduro, V.B., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
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1 (bases 1 to 146144)
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AC138446.2 GI:28209439
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/db_xref="taxon:10090"
/chromosome="9"
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6: contig of 2340 bp in length
6: gap of 100 bp
7: contig of 22221 bp in length
7: gap of 100 bp
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1: gap of 100 bp
9: contig of 16918 bp in length.
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Pred. No. 5.2e-10;
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                                                                                                                                                                                                                                                                           Grovemont Circle, Gait 3 (bases 1 to 146144)
                                                                                                                                                                                                                                                                                              Submitted (03-JAN-2003) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                      Green, E.D.
Direct Submission
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Center project name: dzm
Center clone name: 556K17
                                       Contact: nisc_zoo@nhgri.nih.g
                                                                                   Web site: http://www.nisc.nih.gov
                                                                                                      Center: NIH Intramural Sequencing Center code: NISC
                                                                                                                                                Genome Center
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicate order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, he sequence assembly is based on at least 8x average the sequence assembly is based on at least 8x average. indicated

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 145261 bases at least Q40
Consensus quality: 145617 bases at least Q30
Consensus quality: 145697 bases at least Q30
Consensus quality: 145697 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 145744; sum-of-contigs
Quality coverage: 9.18x in Q20 bases; agarose-fp
Quality coverage: 8.95x in Q20 bases; sum-of-contig sum-of-contigs It currently

source misc\_feature \* by the finished sequence as soon as it is available and the accession number will be preserved.

\* the accession number will be preserved.

\* 11576 contig of 11576 bp in length 11576 to unknown length 11677 11676; gap of unknown length 11677 74352; contig of 62676 bp in length 11673 74452; gap of unknown length 117453 79922; contig of 4470 bp in length 1175923 117514; gap of unknown length 117515 11751 is believed to be correct as given, ho of the gaps between them are based on provided by the submittor.
This sequence will be replaced NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces /note="assembly\_fragment
missing T7 clone end on
11677. .74352 /organism="Pelis catus" /mol\_type="genomic DNA" /db\_xref="taxon:9685" /clone="RP86-556K17" 1. .146144 clone\_ lib="RP86" /Qualifiers ú end however the sizes on estimates that have of f

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Submitted (18-DEC-2002) NIH Intramural Sequencing Center, & Grovemont Circle, Gaithersburg, MD 20877, USA
On Dec 18, 2002 this sequence version replaced gi:25167123
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-NOV-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 139245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulles, E.H., Masiello, C., Maskeri, B., McDowell, J., Maguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Paguirigan, C., Pearson, R., Fortnoy, M.E., Prasad, A., Reddix, Dugue, N., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2; HTGS_DRAFT Felis catus (cat) Felis catus
The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indica order and orientation of each sequence contrig has been established using one or more of the following: read-pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Felis catus clone RP86-386P20,
                                                                                                                                                                                                                                                                                                                                                                    Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1. (bases 1 to 139245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 139245)
                                                                                                        Center project name: dzt
Center clone name: 386P20
                                                                                                                                              Center: NIH Intramural Sequencing Center code: NISC
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clone_end:SP6
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74453. .78922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142715. .146144
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                                                                                                                                                                                                                                                           ---- Genome Center
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78.0%;
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Pred. No. 5.3e-06;
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5-386P20, WORKING
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DRAFT SEQUENCE, 9 ordered
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                                          the indicated
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data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that I provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemietry. Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.990319 consensus quality: 137738 bases at least Q30 consensus quality: 138103 bases at least Q30 consensus quality: 138333 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7979
8079
10290
10390
41760
41860
66913
67013
68183
69343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 125000; agarose-fp
Insert size: 138445; sum-of-contigs
Quality coverage: 9.74x in Q20 bases;
Quality coverage: 8.80x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86962
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69443. .86961
                                                                                                                                                                                                                                                                                            clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                    /note="clone overlaps with GenBank Accession Number AC137541 clone RP86-558L14 (center project name dzs)"
                                                                                                                                               41860
                                                                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Felis catus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                 note="assembly_fragment"
                                                                note="assembly_fragment"
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                                                                                                                                                                                                0390. .41759
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_xref="taxon:9685"
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96862: contig of 9801 bp in 1
96962: gap of unknown length
139245: contig of 42283 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on number will be preserved.
7978: contig of 7978 bp in length
8078: gap of unknown length
10289: contig of 2211 bp in length
10389: gap of unknown length
41759: contig of 31370 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68182: gap of unknown length 69342: contig of 1160 bp in length 69442: gap of unknown length 86961: contig of 17519 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67012: gap of unknown length 68082: contig of 1070 bp in
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66912: contig
                                                                                                 .68082
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of 25053 bp in
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sum-of-contigs
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AUTHORS
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AC137541/c
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Best Local S
Matches 65
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                      The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition,
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-DEC-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Dec 18, 2002 this sequence version replaced gi:25167124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-NOV-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 142025)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, B.D.
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Akhter, N., Antonellis, A.,
the sequence assembly is based on at least 8X average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC137541 142025 bp DNA linear HTG 18-DEC-2 Felis catus clone RP86-558L14, WORKING DRAFT SEQUENCE, 3 ordered
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                                                                                                                                                                                                                  Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
------ Project Information
Center project name: dzs
Center clone name: 558L14
                                                                                                                                                                                                                                                                                                                                         Center: NIH Intramural Sequencing Center code: NISC
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96963. .139245
/note="assembly_fragment
clone_end:T7
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Pred. No. 1.5e-05;
0; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                  Center
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ACCESSION
VERSION
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                                                                                                                                               RESULT 10
AC144468
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                                                                                                                                                                                                                                                                                                                                          70 GCAGCTGTTGATTCCACAGAGGTGAGT 96
                                                                                                                                                                                                                                                                                                                                                                          65;
AC144468 GI:31072038
AC144468.2 GI:31072038
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                  AC144468 144218 bp Canis familiaris clone RP81-263K15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                            ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                 GCAGCTGTTGATTCTGTTAATGTAAGT 115334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and the accession number will be preserved.

1 7831: contig of 7831 bp in length
7832 7931: gap of unknown length
7932 71572: contig of 63641 bp in length
71573 71672: gap of unknown length
71673 142025: contig of 70353 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 141628 bases at least Q40
Consensus quality: 141751 bases at least Q30
Consensus quality: 141818 bases at least Q30
Consensus quality: 141818 bases at least Q20
Insert size: 130000; agarose-fp
Quality coverage: 12.59x in Q20 bases; sum-of-contigs
Quality coverage: 11.54x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:right"
95993_.142025
/note="Clone overlaps with GenBank Accession Number
AC137540 clone RP86-386P20 (center project name dzt)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
7932. .71572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71673. .142025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:9685"
/clone="RP86-558L14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="RP86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Felis catus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51.8; DB 2
Pred. No. 1.5e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                     DNA linear HTG 24-MAY-2003
WORKING DRAFT SEQUENCE, 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 142025;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 144218)
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Elakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Harle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Legaspi, R., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, M., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On May 24, 2003 this sequence version replaced gi:30039737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-APR-2003) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 144218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
by the finished sequence as soon as it is available the accession number will be preserved.

1 67547: contig of 67547 bp in length 67548 67647: gap of unknown length 84498: contig of 16851 bp in length
                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 144218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 143361 bases at least Q40 Consensus quality: 143624 bases at least Q30 Consensus quality: 143760 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc zoo@nhgri.nih.go.
                                                                                                                                                                                                                                                                                                                                                                        Insert size: 130000; agarose-fp
Insert size: 143818; sum-of-contigs
Quality coverage: 11.72x in Q20 bases; agarose-fp
Quality coverage: 10.59x in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: NIH Intramural Sequencing Center Center code: NISC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- Summary Statistics
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AC144469
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54898 TTCACGAAATGTAAGT 54913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 TTCCACAGAGGTGAGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.M., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Glan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, B.H., Massiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Metherby, K.D., Wiggins, L., Young, A. and Green, B.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS PHASE2; HTGS DRAFT Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC144469 223041 bp DNA linear HTG 29-
Canis familiaris clone RP81-354N9, WORKING DRAFT SEQUENCE,
           Submitted (22-APR-2003) NIH Intramural Sequencing Center, 8717
                                      Direct Submission
                                                             Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC144469.2 GI:31126656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ordered pieces
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                                                                                          (bases 1 to 223041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 223041)
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105762
105862
120568
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clone_end:SP6
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84599. .105761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
105862. .120567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .861
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/db_xref="taxon:9615"
/clone="RP81-263K15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120668. .144218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .67547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 50.4; DH 2;
Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end of insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gross misassembles, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 222277 bases at least Q30

Consensus quality: 222424 bases at least Q30

Consensus quality: 222497 bases at least Q20

Insert size: 185000; agarose-fp

Quality coverage: 11.10x in Q20 bases; sum-of-contigs

Quality coverage: 9.22x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * by the finished sequence as soon as it is available and
the accession number will be preserved.

12784: contig of 12784 pp in length
12785 12884: gap of unknown length
12885 81039: contig of 68155 bp in length
81040 81139: gap of unknown length
127412: contig of 46273 bp in length
127413 127512: gap of unknown length
127513 153408: contig of 25896 bp in length
1253409 153508: gap of unknown length
153509 220941: contig of 67433 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicatorder and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 223041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       220942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.nisc.nih.gov
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                                               vector_side:left"
                                                                                                 clone_end:T7
                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:9615"
/clone="RP81-354N9"
/note="assembly_fragment'
                                                                                                                         note="assembly_fragment
                                                                                                                                                                                                                                                                                                                   organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TTCCACAGAGGTGAGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 156655)
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Elakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Hurle, B., Idol, J.R., Karlins, E., Kongy, P., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Taipouri, V., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. Misc Comparative Sequencing Initiative
                                                                                                                                                                               Submitted (17-JUN-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 17, 2003 this sequence version replaced gi:30349002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS PHASE2; HTGS_DRAFT Canis familiaris (dog)
Canis familiaris
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                                                                                                                                                                                                                                                                                                                        Submitted (03-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris clone RP81-249M20,
                                                                                                                                                                                                                                                                                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ordered pieces.
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                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Similarity 78.9%;
                                                                                                                                                                                                                                                                                                (bases 1 to 156655)
                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 156655)
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Center project name: eab
Center clone name: 249M20
                                           Contact: nisc_zoo@nhgri.nih.gov
                                                                                                              Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                         Web site: http://www.nisc.nih.gov
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clone_end:SP6
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221042. .223041
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153509. .220941
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135818. .223041
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AC144468 clone RP81-263K15 (center project name dgz)"
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127513. .153408
                                                                                                                                                              Genome Center
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Pred. No. 4.6e-05;
0; Mismatches 16;
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence
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This sequence will be replaced
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1 920: contig of 9220 bp in length 9221 9320: gap of unknown length 1 9320: gap of unknown length 1 9321 35019: contig of 25699 bp in length 1 9320 35119: gap of unknown length 1 9054; contig of 13935 bp in length 1 9055 49054; contig of 13935 bp in length 1 9055 49154: gap of unknown length 1 9155 73429: contig of 24275 bp in length 1 9156655; contig of 83126 bp in length 1 9156655; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the
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Consensus quality: 155899 bases at least Q40
Consensus quality: 156114 bases at least Q30
Consensus quality: 156199 bases at least Q20
Insert size: 140000; agarose-fp
Insert size: 15625; sum-of-contigs
Quality coverage: 16.25x in Q20 bases; sum-of-contigs
Quality coverage: 14.56x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73530. .156655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="clone overlaps with GenBank Accession Number
AC144470 clone RP81-355L14 (center project name eaa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9615"
/clone="RP81-249M20"
/clone_lib="RP81"
                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment
nissing T7 clone end on 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
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                                                                                                                                                                                            20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _type="genomic DNA"
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                                                                                                                                               Score 50.2; DB 2;
Pred. No. 5.2e-05;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                        end of insert"
                                                                                                                                                                                                                                        Length 156655;
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                                                                                                                                                                                                                                   Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (22-APR-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 208456)
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                                                                                                                                                                                                          On May 23, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                      Green, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC144470.2 GI:31044312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGCTGTTGATTCTGTTAATGTAAGT 126219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGCTGTTGATTCCACAGAGGTGAGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 208456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 208456)
                                            Center: NIH Intramural Sequencing Center code: NISC Center code: NISC Web site: http://www.nisc.nih.gov Contact: nisc zoo@nhgri.nih.gov
Center project name: eaa
Center clone name: 355L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             470 208456 bp I
familiaris clone RP81-355L14,
                                                                                                                                                                                                                                                                                                   Submission
                                                                                                                                                                                         Genome Center
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a branderiad resistance. with a Phrap-derived quality score. Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.99019 Consensus quality: 206358 bases at least Q40 Consensus quality: 207013 bases at least Q30 Consensus quality: 207414 bases at least Q20 100% of reads

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                                                                                                                                                Query Match
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                                                                                                                              Local
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the accession number will be preserved.

1 36929: contig of 36929 bp in length
36930 37029: gap of unknown length
37030 85159: contig of 48130 bp in length
85160 85259: gap of unknown length
85260 139957: contig of 54698 bp in length
139958 140057: gap of unknown length
140058 143501: contig of 3444 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
                                                          CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working consists of 9 contigs. Ga
                                     CCTTTTTAATÄGGCCACATTTÄAGGGATGGATGGATATAATGTÄTGCAGCAGTTGATTCC 71007
ACAGAGGTGAGTCAGTGTTCTACCATG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178630
203002
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160353
164594
164694
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37030
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143502
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                                                                                                               Conservative
                                                                                                                                                                                                   clone_end:SP6
vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone overlaps with AC144605 clone RP81-249M20
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missing T7 clone end on
                                                                                                                                                                                                                                                                                                  178630. .20300
                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment"
143602. .160252
                                                                                                                                                                                                                                                                                                                                                                                                                                                     140058. .143501
                                                                                                                                                                                                                                                                                                                                                                           160353. .164593
                                                                                                                                                                                                                                                                       note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
164694. .178529
                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment"
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130279. .208456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment'
35260. .139957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RP81"
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/clone="RP81-355L14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Canis familiaris"/
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                                                                                                                                                                                                                                        note="assembly_fragment
                                                                                                                                                                                                                                                                                                          note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160352: gap of unknown length
164593: contig of 4241 bp in length
164693: gap of unknown length
178529: contig of 13836 bp in length
178629: gap of unknown length
203001: contig of 24372 bp in length
203101: gap of unknown length
203101: gap of unknown length
208456: contig of 5355 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143601: gap of
160252: contig
                                                                                                                          20.6%;
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                                                                                                             0
                                                                                                         Score 50.2; DB 2;
Pred. No. 5.3e-05;
D; Mismatches 23;
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lg of 16651 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenBank Accession Number (center project name eab)"
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                                                                                                                                              Length 208456;
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AC117294
LOCUS
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ORGANISM
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HTG; HTGS PHASE1; HTGS DRAFT;
Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-251M17, WORKING DRAFT SEQUENCE, 2
Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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Direct Submission
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HASE1; HTGS_DRAFT; HTGS_FULLTOP
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FEATURES
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Matches
                            Query Match
Best Local Similarity
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On Oct 10, 2002 this sequence version replaced gi:21745888.
On Oct 10, 2002 this sequence version replaced gi:21745888.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Sequencing Consortium Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-251M17

Center clone name: CH230-251M17

Center clone name: CH230-251M17

Center Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 188626 bases at least Q40

Consensus quality: 188678 bases at least Q20

Consensus quality: 189677 bases at least Q20

Estimated insert size: 191689; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://
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Conservative
                                                                                                                                                                                 clone_end:T7
site:MboI
                                                                                                                                                                                                                                                                         /note="wgs_contig"
complement(199245.
                                                                                                                                              end_sequence:RXABQ81TJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                             /note="clone_boundary
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                            20.2%;
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                         Score 49.2; DB 2;
Pred. No. 0.00011;
Mismatches
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18;
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Gaps
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TTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCAC 86

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JOURNAL REFERENCE
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                                                                                                                                                                                                             RS Muzny, D. Marie, Metzker, M. Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalbechi, V., Avyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ccasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockell, R., Cox, C., Coyle, M., Cyce, A., D. Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinhi, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Engene, C., Evans, C.A., Falls, T., Foater, M., Fraser, C., M., Gabisla, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Foater, M., Genrarane, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Lorensuhewai, L., Loulseged, H., Lozado, R. J., Lu, X., Mangum, B., Howells, S., Hulyk, S., Hume, J., Tdlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Ke
Direct Submission Unpublished 2 (bases 1 to 232282)
                                                                                             Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,G., Yen,J., Yoon,L., Yoon,V Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC094738.4 GI:30466565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGGTGAGTCAGTGTTC 104
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232282 bp
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WORKING DRAFT SEQUENCE.
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REFERENCE AUTHORS

JOURNAL TITLE AUTHORS TITLE

Worley, K.C. Direct Submission

JOURNAL

COMMENT

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FEATURES
                                                                                                                                               misc_feature
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3 (bases 1 to 232282)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:22771706.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') Within each contig-scaffold, assembly (a 'contig-scaffold') Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 232282: contig of 232282 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GBGN

Center clone name: CH230-5C5

Center clone name: CH230-5C5

Assembly program: Atlas;

Consensus quality: 213583 bases at least Q40

Consensus quality: 216581 bases at least Q20

Consensus quality: 21872 bases at least Q20

Consensus quality: 21872 bases at least Q20

Betimated insert size: 227971; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
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                                      /note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                           23535. .25164
/note="wgs contig"
complement(229031. .229780)
                                                                                                                                                                                                                                                                                                   /note="clone_boundary clone_end:Sp6 site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="CH230-5C5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                    sequence:BH334717"
_sequence:BH334716"
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ORIGIN

밁 ঠ 밁 Ś Matches Query Match Best Local 7203 TIGTTTCCAGGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCCGG 7262 7263 AGAGGTGAGCCCCGGCTC 7280 87 AGAGGTGAGTCAGTGTTC 104 27 TTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCAC 86 60; Similarity Conservative 20.2%; .. Score 49.2; DB 2; Pred. No. 0.00011; Mismatches DB 2; Length 232282; Gaps 0

Search completed: March 22, 2004, 19:32:40 Job time: 1304.82 secs

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47

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Minimum DB Maximum DB
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No.
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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and is
                                                                                                                                                                                                                               Score
244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
                                                                                                                                                                                                                                                                             No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic search, using sw
                                                                                                                                                                                                   100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3373863 seqs, 2124099041 residues
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244
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geneseqn2002s:*
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geneseqn2000s:*
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                                                                                                                                                                                                                               Length
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                               DB
AAH55818
AAX6022
AAX87602
AAF30104
AAF30104
AAF32750
AAF30103
AAF57016
AAH557016
AAK12409
                                                                                                                                                                                                   AAZ21492
AAH55850
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                         Aaz21492 Human sen
Aah55818 Human SCN
Aah55818 Human SCN
Aax60242 cDNA enco
Aax87602 Human sod
Aaf30104 Human sod
Aaf30101 Human sod
Aaf30101 Human sod
Add32193 Human sod
Add32193 Human sod
Aah55788 Human SCN
Aai66961 Human SNS
Aai66961 Human hPN
Abx13103 Human nco
Abx13103 Human pN3
Abx13103 Human pN3
Ada50151 Human pN3
Ada50151 Human per
Aas31089 Human dia
Aai66959 Rat SNS1
Aai66959 Rat SNS1
Aai66959 Rat SNS1
Aai66959 Rat SNS1
         Aas31089
Aai66959
Aaf57009
Abx12402
Ada50143
                                                                                                                                                                                                                               Description
        cDNA enco
Rat perip
cDNA enco
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36.2		36.2				37.2	37.2		37.2	37.2	40.2		40.2			40.2		41.2			41.2
		14.8			15.1	15.2	15.2	15.2	15.2	15.2	16.5	16.5	16.5	16.5				16.9			16.9
5997	5997	5946	5922	5889	6822	8509	8490	6957	6048	6048	9123	9112	9112	6599	6599	6599	6596	7052	6606	6527	6524
9	σ	ø	σ	6	σ	7	δ	ø	4	N	6	IJ	ഗ	9	9	9	9	N	N	N	7
ACF57879	AAD32839	ACF57880	AAD32845	AAD32840	ABK63697	ACC46433	ABZ35506	ADB52723	AAF30825	AAV09029	ABL39690	AAH55824	AAH55823	ADB78647	ADB78648	ADB78650	ADB78646	AAT77805	AAX60872	AAT77806	ABX13101
Acf57879	Aad32839	Acf57880	Aad32845	Aad32840	Abk63697	Acc46433	Abz35506	Adb52723	Aaf30825	Aav09029	Ab139690	Aah55824	Aah55823	Adb78647	Adb78648	Adb78650	Adb78646	Aat77805	Aax60872	Aat77806	Abx13101
Human SCN	Human ion	Human SCN	Human ion	Human ion	Rat seque	Human dit	Human gen	Primary r	Human SCN	Human hH1.	Human sod	Human neo	Human adu	Human ion	Human ion	Human ion	Human ion	cDNA enco	NaNG poly	cDNA enco	Rat cDNA

## ALIGNMENTS

Human sensory neurone specific 2a nucleotide sequence fragment #12

03-DEC-1999 AAZ21492;

(first entry)

RESULT 1

AAZ21492 standard; cDNA;

244

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AAZZ1492
XX
XX
AC AAZZ
AC AAZZ
AC AAZ
CC Bpe
CC modd
CC modd
CC med
XX
Sec
                                                                                                                                                                                                                                                                               Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
                                                                                                                          WPI; 1999-562112/47.
                                                                                                                                            Grose DT, Hick CA,
                                                                                                                                                                                                                                           WO9947670-A1
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                   Claim 6; Page 67; 73pp; English.
                                                                                                       Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                                  18-MAR-1998;
                                                                                                                                                                                                    18-MAR-1999;
                                                                                                                                                                                                                       23-SEP-1999.
                                                                                                                                                               (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                   98GB-00005793.
                                                                                                                                                                                                      99WO-GB000838.
                                                                                                                                             Tate
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Query Match Best Local Similarity Matches 244; Conserv

Conservative

100.0%; Score 244; DB 2; 100.0%; Pred. No. 1.5e-68; tive 0; Mismatches 0;

Length 244; Indels

0,

Gaps

0

Sequence 244 BP; 58 A; 49 C; 57 G; 80 T; 0 U; 0 Other;

for the treatment of pain or hypersensitivity

AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a

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ARESULT 2
AAH55885
AC AAH5
AC 
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                                                       The present invention describes a method (M1) of determining an individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The method comprises determining the genotype of at least one gene selected from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium channel genes located on chromosome 2. The idiopathic generalised epilepsy (IGE) gene is more specifically localised on chromosome 2g3-q31. Compounds identified as modulators of the biological activity of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AMH55763 to AMH56164 and AMB99674 to AMB99679 represent SCN1A, SCN2A, and SCN3A CDNAB, gene fragments, PCR primers, oligonucleotides and proteins given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification; diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining a predisposition to epilepsy and/or development of epilepsy comprises determining the genotype of SCNIA, SCN2A and/or SCN3A, or a D variant, equivalent, or mutation which shows a linkage disequilibrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human SCN3A genomic DNA fragment SEQ ID NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH55850 standard; DNA; 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 183; 268pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rouleau GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-2000; 2000WO-CA001404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMC-) UNIV MCGILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ч
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTATGGTCAAGTCAGAGATATCATGACTACATGGACAGTCCAGAACTGGCGTCATAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGTTTATGCAGCTGTTGATTCCACAGAGGTGAGTCAGTGTTCTACCATGTTCGGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lafreniere RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rochefort D, Cossette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ragsdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
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RESULT 3
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                                                           The present invention describes a method (M1) of determining an CC individual's predisposition to epilepsy and/or development of epilepsy, and/or development of epilepsy, and/or development of epilepsy, and/or development of epilepsy, and sevelopment of epilepsy, and sevelopment of epilepsy, and sevelopment of epilepsy, and sevelopment of epilepsy, as well as predicting the genotype of at least one gene selected from CC scNlA, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium CC channel genes located on chromosome 2. The idiopathic generalised CC epilepsy (ICE) gene is more specifically localised on chromosome 2q23-CC epilepsy (ICE) gene is more specifically localised on chromosome 2q23-CC epilepsy (ICE) gene is more specifically localised on chromosome 2q23-CC compounds identified as modulators of the biological activity of CC compounds identified as modulators of the biological activity of CC or other neurological disorders. They have anticonvulsant and CC or other neurological disorders. They have anticonvulsant and CC or other neurological disorders. They have anticonvulsant and CC or other neurological disorders. They have anticonvulsant and CC or other neurological disorders of the present CC of the convulsant and convulsant and CC or other neurological disorders. They have anticonvulsant and CC or other neurological disorders of the present CC of the convulsant and convulsant a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining a predisposition to epilepsy and/or development of epilepsy comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DI variant, equivalent, or mutation which shows a linkage disequilibrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification; diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH55818 standard; DNA; 480
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                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 148; 268pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-355945/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rouleau GA, Lafreniere RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-2000; 2000WO-CA001404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human SCN2A genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH55818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMC-) UNIV MCGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 ATTATGTATGCAGCTGTTGATTCACGAGATGTAAGT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0167623P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA fragment SEQ ID NO:60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 65 G; 166 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rochefort D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cossette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ragsdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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Query Match Best Local S Matches 57

Local Similarity nes 57; Conserv

BP;

172

A; 59 Ç

64 G;

185 T; 0 U; 0 Other

Conservative

0

19.4**%**; 78.1**%**;

Score 47.4; DB 5; Pred. No. 5.5e-05;

Length 480; Indels

0

Gaps

0,

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RRESULT 4
AAX60242
IID AAX60
XX AAX6
XX AAX6
XX AAX6
XX AAX6
XX AAX6
XX CDNA
XX Type
XM diab
XX Inm

  RESULT 5
AAX87602
ID AAX8
XX
AC AAX8
XC AAX8
XX
DT 26-0
XX
Huma
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                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                         26-0CT-1999
                                                                                                             AAX87602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 856 BP; 251 A; 172 C; 170 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 3A; 90pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY16577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dietrich PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuropathic pain; migraine; headache; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding type 5 sodium channel protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX60242 standard; cDNA; 856
Human sodium channel NaN partial cDNA.
                                                                                                                                                                    AAX87602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                     GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAG 90
                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding sodium channel of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAAATGTAAGTC 238
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                                                                                                                                                                                                                                                                                                           GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fish LM,
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                                                                                                                                                                    CDNA; 3638
                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 9.2e-05;
0; Mismatches 5;
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CDS

Location/Qualifiers
1. .3699

Homo

hyperexcitability; Sodium channel;

NaN; human; tetrodotoxin resistant; pain; paraesthesia; ty; analgesic; vaccine; gene therapy; diagnosis; ss.

analgesic; vaccine; gene therapy;

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RESULT 6
AAF30104
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other modifying the behaviour of these nerve cells while not affecting other modifies the behaviour of these nerve cells while not affecting other modifies the behaviour of these nerve cells while not affecting other modifies the behaviour of these nerve cells while not affecting other modifies the behaviour of these nerves cells while not affect the modifies the behaviour of these nerves cells while not affect the modifies the behaviour of these nerves cells while not affect the modifies the modifies the behaviour of these nerves cells while not affect the modifies the modifie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                        30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3638 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 8A1-2; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dib-Hajj S, Waxman
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20-NOV-1998;
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Human sodium channel NaN partial cDNA.
                                                                                                                                                                                                                                                                          AAF30104;
                                                                                                                                                                                                                                                                                                                                                                                                     AAF30104 standard; cDNA; 3701 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cells in the brain and spinal cord. The gene is named SCN11a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06598
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                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ß
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Pred. No. 0.00016;
0; Mismatches 5
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ARL42750
ID AAL42750
ID AAL4
XX AAL4
XX AAL4
XX 19-J
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium CC channel protein family and produces a TTX-R sodium current. Such channels CC underlie the generation and propagation of impulses in excitable cells CC such as neurons and muscle fibres. Preferential expression of NaN on CC sensory neurons innervating the body (dorsal root ganglia) and the face CC (trigeminal ganglia), but not on other neurons, makes it a very useful CC target for diagnostic and/or therapeutic uses in relation to acute and/or CC chronic pain pathologies. A claimed method of treating pain, paraesthesia CC and/or hyperexcitability phenomena in a human or animal subject involves CC daministering an agent that alters sodium current flow through NaN CC channels, or which modulates transcription or translation of NaN mRNA, in CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in CC channel expression or (antisense) to down-regulate NaN expression, in the CC diagnosis of disease, and in the recombinant production of NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-1999;
                                                                          Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; thuman nervous system; chromosome 3p23-21.3; excitatory cell drug development; familial hyperglycaemia; QT extending sync
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a partial cDNA for a novel human tetrodotoxin resistant sodium channel, termed NaN (see AAB20125). The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). A full-length sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dib-Најј S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-US019342.
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                                                          motor endplate disease.
                                                                                                                                                      Human sodium channel subunit SCN12A-s coding sequence.
                                                                                                                                                                                                19-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                           AAL42750 standard; cDNA; 5728 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 8A; 162pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                         GCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                              syndrome type
                                                                                                                      SCN8A;
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Homo

sapiens

14-JUL-2000; 2000WO-US019342

25-JAN-2001.

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RESULT 8
AAF30101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A-s sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human sodium channel NaN cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF30101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 55-70; 118pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2000; 2000JP-00152085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                         Location/Qualifiers 31. .5402
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90.9%;
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Pred. No. 0.00019;
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RRESULT 9
ADD32193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of cDNA encoding a novel human tetrodotoxin CC resistant sodium channel, termed NaN (see AAB20121). The cDNA was CC isolated from a human dorsal root ganglia tissue cDNA library by PCR CC seplated from a human dorsal root ganglia tissue cDNA library by PCR CC amplification (see also AAB20122-23). NaN belongs to the a-subunit CC current. Such channels underlie the generation and probagation of CC current. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres.

CC Preferential expression of NaN on sensory neurons innervating the body CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic CC uses in relation to acute and/or chronic pain pathologies. A claimed CC method of treating pain, paraesthesia and/or hyperexcitability phenomena CC in a human or animal subject involves administering an agent that alters CC sodium current flow through NaN channels, or which modulates CC trigeminal neurons. NaN nucleic acids are used in gene therapy to correct CC disorders associated with decreased sodium channel expression or CC (antisense) to down-regulate NaN expression, in the diagnosis of disease, CC and in the recombinant production of NaN polypeptides
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Best Local S
Matches | 50
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20-MAR-2002; 2002US-0365550P
                                                           20-MAR-2003; 2003WO-US008611
                                                                                                                              02-OCT-2003.
                                                                                                                                                                                          WO2003080570-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron; human; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD32193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUL-1999;
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50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 5860 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG 3843
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                     /product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                                                                                                                          /*tag=
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J.00019;
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RESULT 10
AAL42749
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a human Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.
                                                                                                              CDS
                                                                                                                                                                                                         Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; human nervous system; chromosome 3p23-21.3; excitatory cell; drug development; familial hyperglycaemia; QT extending syndrome type motor endplate disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3; 125pp; English.
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                  19-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                       AAL42749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                         channel subunit SCN12A coding sequence
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                            Location/Qualifiers 200. .5575
                                                                         /product= "Human sodium channel subunit SCN12A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                       Determining a predisposition to epilepsy and/or development of epilepsy comprises determining the genotype of SCNIA, SCN2A and/or SCN3A, or a DI variant, equivalent, or mutation which shows a linkage disequilibrium.
                                                                                                                                                                                                                                                                                                                           Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification; diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN1
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                                                                                                                 Rouleau GA,
                                                                                                                                                                                                      24-NOV-2000; 2000WO-CA001404
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                                                                                                                                                                                                                                                                 WO200138564-A2
                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH55788 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;
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                                                                                                                                              (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-393394/42.
                                                                                                                                                                                                                                                                                                                                                                                    SCN1A genomic DNA fragment SEQ ID NO:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG 4012
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto J,
                                                                                                                 Lafreniere
                                                                                                                                                                            99US-0167623P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeong S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
                                                                                                                 RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 6;
Pred. No. 0.0002;
0; Mismatches
                                                                                                                  Rochefort
                                                                                                                 á
                                                                                                                 Cossette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6528;
                                                                                                                 Ragsdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT 12
AA166961
ID AA166
AC AA166
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AC AA166
XX ION C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The method comprises determining the genotype of at least one gene selected from SCNIA, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium channel genes located on chromosome 2. The idiopathic generalised epilepsy (IGE) gene is more specifically localised on chromosome 2q23-q31. Compounds identified as modulators of the biological activity of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers, oligonucleotides and proteins given in the exemplification of the present inventor.
                                                       Altered ion channel protein useful for screening modulators that are useful in the manufacture of a medicament for the treatment of pain, inflammation and hypersensitivity, has acquired sensitivity to gating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ion channel protein; gating; sensory neurone specific protein;
analgesic; antiinflammatory; immunosuppressive; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI66961 standard; DNA; 5874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 114; 268pp; English
                                                                                                                                                                                                                                                                    Aitken AJ,
                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2000; 2000GB-00006024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2001; 2001WO-GB001108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200168681-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human SNS1 ion channel protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI66961;
                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a method (M1) of determining
                                                                                                                                                                                                               2001-590038/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                AAG65785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAGAGGTGAGTCAGTGTTCTA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTCTTAATAGGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAATGTAAGTATTCCTTGTA 273
                                                                                                                                                                                                                                                                       Chen MX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 170 A; 60 C; 69 G; 158 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "SNS1 ion channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 5871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.2%;
                                                                                                                                                                                                                                                                    Gladwell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 5;
Pred. No. 0.003;
                                                                                                                                                                                                                                                                          ΣM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                          Powell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                          AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 457
                                                                                                                                                                                                                                                                          Tate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                             pain,
gating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Disclosure; Page

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RESULT 13
AAPS7016
ID AAPS7016
ID AAPS7016
AC AAPS
XX AAPS
XX AAPS
XX Peril
KW Eeril
KW sodil
KW sodil
KW anal
XX Home
                                  New rat and human tetrodotoxin-resistant, voltage-gated proteins, present in peripheral nerve tissue, useful as target for compounds treating peripheral nervous system
                                                                                    sodium channel
a therapeutic
                                                 disorders.
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compound

Herman

'n

Delgado SG,

SYNTEX USA

2001-202004/20.

AAB61996.

11-OCT-1995; 15-APR-1997; 06-FEB-2001. US6184349-B1

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sensitivity to a gating agent. The altered ion channel protein can be expressed by standard recombinant methodology. The altered ion channel protein can be derived from a rat, mouse or human unaltered, gating agent insensitive ion channel proteins. The altered protein is useful in screening assay for the identification of modulators capable of modulators and unaltered gating agent insensitive ion channel protein. The modulator identified by the assay is preferably an antagonist of the altered protein, which is useful in the manufacture of a medicament for the treatment of pain, inflammation or hypersensitivity, and for treating a manmalian patient, particularly human. The present sequence represents a DNA encoding a human sensory neurone specific (SNS) 1, a sodium ion than the protein that the sequence represents the protein and the protein that the protein that the protein that the particularly human the protein that the prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tetrodotoxin; TTX; peripheral nerve sodium channel type 3; PN3; human; sodium channel protein; peripheral nervous system; allodynia; neuropathy; hyperalgesia; traumatic injury; antidiabetic; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peripheral nerve tetrodotoxin-resistant sodium channel alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides an altered ion channel protein having acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 5874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTCCCGGGAGGTCA 4147
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72.0%;
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Pred. No. 0.012;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                    Sangameswaran
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RESULT 14
ABX13103
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XX ABX13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nerve tetrodotoxin (TTX)-resistant sodium channel alpha subunit proteins. The rat peripheral nerve sodium channel type 3 (PN3) protein or its human homologue are useful for the development of antibodies against PN3 which are useful in affinity chromatography to purify recombinant sodium channel proteins or polypeptides, or as a research tool. The PN3 proteins are useful as therapeutic targets for compounds to treat disorders of the peripheral nervous system such as allodynia, hyperalgesia, diabetic neuropathy, traumatic injury and acquired immunodeficiency syndrome (AIDS) associated neuropathy. The present sequence represents the cDNA proteins are the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  small calcium binding protein; analgesia; chronic pain; osteoarthritis; rheumatoid arthritis; neuropathic pain; cancer pain; tri geminal neuralgia; hyperalgesia; inflammatory pain; nociceptive pain; tabes dorsalis; phantom limb pain; spinal cord injury pain; central pain; post-herpetic pain; HIV pain; non-cardiac chest pain; irritable bowel syndrome; bowel disorder.
                                    Identifying a voltage gated sodium channel (VGSC) modulator for producing analgesia and for relieving chronic pain, e.g. osteoarthritis or HIV pain, comprises bringing into contact a VGSC, a pl1 peptide and a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5874 BP; 1434 A; 1553 C; 1428 G; 1459 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001; 2001GB-00020238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003016917-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2002; 2002WO-GB003852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding voltage-gated sodium channel Nav1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 2041. .5871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Nav1.8"
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                                                                                                                                                                                                                                                                                                                                                        Poon L,
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72.0%;
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                                                                                                                                                                                                                                                                                                                                                             Malik-Hall
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Homo

sapiens

/\*tag= a

.5871

analgesic;

anti-HIV;

88.

Human 14-MAY - 2001 AAF57016; AAF57016

hPN3 cDNA sequence.

(first entry)

Query Match Best Local S Matches 54

Similarity

0

4132 79 0

54;

Conservative

Sequence 5874 BP; 1434 A;

channel protein

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ABX12409
ID ABX12
XX ABX12
AC ABX12
XX ABX12
XX OB-MA
XX Human
CAN Sodiu
XM Sodiu
XM Volte
XM Volte
XM Peri
XX PET
CDS
FT CDS
FT CDS
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FT
XX WS64

XX WS64

               US6479259-B1
                                                                                                                                                 Homo sapiens
                                                                                                                                                                       peripheral nerve disorder; gene; ss.
                                             /product= "hPN3"
/note= "Peripheral nerve sodium channel type 3"
/transl_except= (pos:1258. .1260, aa:Glu)
/transl_except= (pos:1534. .1536, aa:Xaa)
/note= "Xaa= Unknown, represented as Arp in the
                                                                                                                          ocation/Qualifiers
                                                                                                                 .587
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The invention relates to identifying a modulator of a voltage gated CC VGSC, a pil peptide (a small calcium binding protein of the S-100 family) CC and test compound (tc) so that the VGSC and the pil peptide can form a CC complex in the absence of the (tc); and (b) measuring an activity of the VGSC, where a change in the activity of the VGSC relative to the activity of in the absence of the (tc); and (b) measuring an activity of the VGSC. Also included are a method of enhancing the functional expression CC vGSC. Also included are a method of enhancing the functional expression CC of a VGSC in a cell by increasing the level of pil in the cell, a CC compound identified by a method above, a host cell capable of expressing a VGSC and a pil peptide (where the VGSC and/or peptide 11 is expressing CC a VGSC and a pil peptide (where the VGSC and/or peptide 11 is expressing CC relating a disorder or condition associated with the cell).

CC compound identified by the method above, a host cell capable of expressing CC compounds identified by the method above, an individual a CC compounds identified as modulator of VGSC are useful for manufacturing a medicament for modulating the functional expression of a voltage gated sodium channel, for producing analgesia and for relativity of pain, tri geminal neuralgia, primary and secondary hyperalgesia, contral pain, tabes dorsalis, phantom limb pain, contral pain, central pain, post-herpetic pain and HIV pain, con-cardiac chest pain, irritable bowel syndrome and pain associated with he pain associated with the pain associated with the pain associated with pain, central pain, post-herpetic pain and HIV pain, con-cardiac chest pain, irritable bowel syndrome and pain associated with bowel disorders. The present sequence encodes the human VGSC Navl.8
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Best Local
Human; peripheral nerve sodium channel type 3; PN3; neuroprotective; sodium antagonist; gene therapy; tetrodotoxin-resistant; TTX-resistant voltage-gated; tetrodotoxin-resistant sodium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 85-95; 114pp; English
                                                                                                                                          cDNA encoding human peripheral nerve sodium channel type 3 (hPN3).
                                                                                                                                                                                                                      08-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                           ABX12409;
                                                                                                                                                                                                                                                                                                                                                            ABX12409 standard; cDNA; 5874 BP
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Pred. No. 0.012;
0; Mismatches 21;
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Matches
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Query Match
                                                                                                                                                                                              The invention describes a purified and isolated polynucleotide (I) encoding a peripheral nerve tetrodotoxin (TTX) resistant sodium channel alpha subunit polypeptide. The methods and compositions of the present invention using voltage-gated tetrodotoxin-resistant sodium channel agents useful for treating peripheral nerve disorders. This sequence encodes the human peripheral nerve tetrodotoxin (TTX)-resistant sodium
                                                                                                                                                                                                                                                                                                                   New purified and isolated voltage-gated tetrodotoxin-resistant sodium channel polynucleotide and encoded polypeptide, useful for treating peripheral nerve disorders.
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15-APR-1997;
                                                                                                                                                         Sequence 5874 BP; 1434 A; 1553 C; 1427 G; 1460 T; 0 U; 0 Other;
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                                                                                                                                                                                     channel type 3 (PN3)
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4133 ATTCCCGGGAGGTCA 4147
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                                                                                                                    Similarity
                                                    ATTCCACAGAGGTGA 94
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                                                                                                        Conservative
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97US-00843417.
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72.0%;
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Pred. No. 0.
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                                                                                                         Mismatches
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                                                                                                                                Length 5874;
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Result
No.
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Maximum DB
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Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                 Pred No. is the number of results predicted by chance to a score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                   37.2
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seq length: 2000000000
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(without alignments)
6039.709 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                       is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
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244
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004. Compugen Ltd.
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/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
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US-10-388-470-41
US-10-220-120-104
US-10-220-120-176-1
US-10-202-824-1
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US-10-202-824-5
US-09-840-125-3
US-09-840-125-3
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US-09-896-994-1
US-10-101-510-617
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Sequence 6, Appli
Sequence 41, Appl
Sequence 104, App
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-10-027	US-10-311-455-13	US-10-027	US-10-027-632-25	US-10-312-841-2	US-09-93	09-930-871-5	9-887-576	-10-243-468-	-10-388-470-	US-10-128-714-5467	-10-128-714-	-10-128-714-	US-10-128-714-1467	-10-128-714-	US-10-128-714-2467	71-	US-09-457-571-1	US-10-311-455-213	-10-204	US-10-297-022-40	US-10-101-510-630	US-10-161-803-60	US-10-388-470-1	US-09-908-975-23882	9-930-871-	-930-	-09-930-871-	US-09-930-871-3
Sequence 117972,			Sequence 250280,	Sequence 2, Appli	15, Appl	Sequence 5, Appli	7	4	4	5	467,	e 6467,	æ	e 7467,	ø			Sequence 213, App		ø	æ	ø	Sequence 1, Appli	e			ø	Sequence 3, Appli

## ALIGNMENTS

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Query Match Best Local Similarity Matches 208; Conser	; LENGTH: 605 ; TYPE: DNA ; ORGANISM: Human ; ORGANISM: 110-027-632-185132	; PRIOR FILING DA ; PRIOR APPLICATI ; PRIOR FILING DA ; NUMBER OF SEQ I ; SOFTWARE: FastS ; SEO ID NO 185132		; TITLE OF I ; TITLE OF I ; CURRENT AL ; CURRENT EI ; PRIOR APPI ; PRIOR FILI ; PRIOR FILI ; PRIOR FILI ; PRIOR FILI	RESULT 1 US-10-027-632-185132/c US-10-027-632-185132, App Sequence 185132, App Publication No. US20 GENERAL INFORMATION: APPLICANT: Wang, Da TITLE OF INVENTION:
vat	605 IA 1: Human 12-185132	S E E		TITLE OF INVENTION: Polymorphisms in the FILE REFERENCE: 108827:129 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 CURRENT PRICATION NUMBER: US 60/218,006 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/193,483	1i
9 # ** **		En 1999-09-28 NUMBER: US 60/146,002 : 1999-08-09 : 1999-88-09 : 1999-08-09 : 1999-08-09 : 1999-09-28 : 1999-09-09 : 1999-09 : 1999-	2000-03-29 NUMBER: US 60/185,218 2000-02-24 NUMBER: US 60/167,363 1999-11-23 1090-02-60/156,358	orphisms: US/10/ -04-30 US 60/21 -12 -12 US 60/19	on US/10027632 075A9
DB 15; e-59; 9; I				in the Human Genome 027,632 8,006 8,676	27632 and Mapping of Single
Length 605; Indels 0;				Φ	gle Nucleotide
Gaps 0					rd. e

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RESULT 3
US-10-388-470-41
US-10-388-470-41
Sequence 41, Application US/10388470
Publication No. US20030228662A1
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-500-10-US
CURRENT APPLICATION UMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR TILING DATE: 1999-07-16
PRIOR PPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR PPLICATION NUMBER: US 60/109,402
PRIOR PPLICATION NUMBER: US 60/109,402
PRIOR PILING DATE: 1998-11-20
PRIOR PPLICATION NUMBER: PCT/US99/02008
PRIOR PPLICATION NUMBER: PCT/US99/02008
PRIOR PILING DATE: 1999-01-29
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: )
OTHER INFORMATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dib-Hajj,
APPLICANT: Waxman,
 PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)..(369
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No.
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SEQ ID NO 41
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NAME/KEY: CDS
LOCATION: (31)..
                                                 APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
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APPLICANT:
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                  CURRENT APPLICATION NUMBER: US/10/220,120 CURRENT FILING DATE: 2002-08-26
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,698; 60/184,770; 60/184,774;
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VU, Jimmy y
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PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION SINGER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                             OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-07-16
3789 GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAG 3843
                                             36 GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAG 90
                                                                                                                     19.3%;
Similarity 90.9%;
                                                                                                  Conservative
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                                                                                               Score 47; DB Pred. No. 5.1e 0; Mismatches
                                                                                                  0;
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CHALUP, MICHALUP, Simon C. INCYTE GENOMICS, INC DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
FONG, Willy T. AMSHEY, Sterming, Christopher COHEN, Wensheng CHEN, Alice D'SA, Steven A. PANZER, Scott R SPIRO, Peter A. BRADLEY, Diana L. BRATCHER, Shawn R. STOCKDREHER, Theresa DAFFO, Abel RUSSO, Frank D ROSEN, Bruce LIU, Tommy F. ROSEBERRY, Ann M. GREENAWALT, Lila B. BANVILLE, Steven C WRIGHT, Rachel J. Application US/10220120 US20040048253A1 Pierre E. Anissa L. Michael S. Jennifer L. ×

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; NAME/KEY: unsure
; LOCATION: 6797, 7046, 7252, 7311, 7325-7326, 7502-7503,
; OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-104
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Best Local
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SEQ ID NO 104
LENGTH: 8530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-17; 2000-02-17; 2000-02-16; 2000-02-16; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10; 2000-05-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:410188.1:2000MAY01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/184, 769; 60/184, 768; 60/184, 837; 60/184, 772; 60/185, 213; 60/1985, 216; 60/204, 815; 60/203, 785; 60/204, 821; 60/204, 525; 60/205, 285; 60/205, 232; 60/205, 324; 60/205, 286
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60/184,769; 60/184,768; 60/184,837;
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                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/209,776
PRIOR APPLICATION: CUNKNOWN>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/511,828 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syntex Corporation, Patent Department A2-200
STREET: 3401 Hillview Avenue P.O. Box 10850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sangameswaran, Lakshmi
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Herman, Ronald C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ATTCCACAGAGGTGA 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 94303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fish, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delgado,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.0%;
72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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; 60/184,697; 60/284,841;
; 60/204,863; 60/205,221;
; 60/204,908; 60/204,226;
; 60/205,323; 60/205,287;
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RESULT 6
US-10-202-824-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                     NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-7466
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-U1-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                  APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: rat
TISSUE TYPE: Dorsal root ganglia
CELL TYPE: Peripheral nerve
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 28340 TELECOMMUNICATION INFORMATION:
                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akopian, Armen N. TITLE OF INVENTION: Ion Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wood, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4163 GGAGAGATCA 4172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Peries, Rohan REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Concord Pike, P.O. Box 15437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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TELEFAX: (415)-496-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
TYPE: nucleic
                 ENGTH: 6524 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZENECA Pharmaceuticals
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74.3%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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Publication No. US20030176648A1
GENERAL INFORMATION:
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  Matches
                                         Query Match
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-7466
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: Floppy disk

COMPUTER: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:

APPLICATION UNDER: US/10/202,824
FILING DATE: 26-UNCHOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 52; Conser
  Local Similarity 74.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals
STREET: 1800 Concord Pike, P.O. Box 15437
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
                                                                                               LOCATION: 204..6077
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                             FEATURE:
                                                                                                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 6527 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akopian, Armen N. TITLE OF INVENTION: Ion Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4347 GGAGAGATCA 4356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4287 CTTCTTCAGGTGGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCC 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 CTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC
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LOCATION: 204..6077
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/669,656 FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                     NAME/KEY: CDS
LOCATION: 204
                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wilmington
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nilarity 74.3%;
Conservative
                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
16.9%; Score 41.2; DB 14; Length 6527; 74.3%; Pred. No. 0.0052; tive 0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.2; DB 14;
Pred. No. 0.0052;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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  Gaps
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NAME/KEY: CDS
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LOCATION: 204..6602
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-202-824-5
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US-10-202-824-5
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                                                                                                                                                                                Query Match
Best Local &
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-7466
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-U1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-UUN-1996
AFTICING DATE: 24-UUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                             4812 CTTCTTCAGGTGGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCC 4871
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                            FEATURE:
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  4872 GGAGAGATCA 4881
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                                     85 ACAGAGGTGA 94
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                                                                                                                                                             l Similarity 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ZENECA Pharmaceuticals STREET: 1800 Concord Pike, P.O. Box 15437 CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                               CTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7052 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                  16.9%;
74.3%;
                                                                                                                                                           Score 41.2; DB 14; Length 7052;
Pred. No. 0.0054;
0; Mismatches 18; Indels 0;
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US-09-840-125-3 ; Sequence 3, Application US/09840125 ; Patent No. US20020061524A1

RESULT 9

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; LOCATION: (1)..(6048)
US-09-840-125-3
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Best Local Similarity
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SOFTWARB: PALENTIN VET. 2.0
SEQ ID NO 3
LENGTH: 6048
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PRIOR APPLICATION NUMBER: 09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,488
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDICATION NO. CONTROL OF THE CONTRO
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APPLICANT: Keatling, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG OT SYNDROME GENES KYLOTI AND
TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2323-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-896-994-1
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CURRENT FILING DATE: 2001-04-24
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ORGANISM: Homo sapiens
INFORMATION
                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/99/896,994

PILING DATE: 02-Jul-2001

CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/514,907

APPLICATION NUMBER: 09/514,907

PILING DATE: cunknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REFERENCE/DOCKET NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

TELECOMMUNICATION INFORMATION:
TPELEDENOW: 1750: E60-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024Alris
STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGAG 90
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                                       TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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RESULT 12
US-10-101-510-617
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; LOCATION: (10)..(6054)
US-10-077-054-1
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                                                                                                                                                                              Sequence 617, Application US/10101510 Publication No. US20030148295A1 GENERAL INFORMATION:
SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local 9
                           APPLICANT: WAN, JACKSON
APPLICANT: WANG, YINN
APPLICANT: WANG, YINN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REPERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR PPLICATION NUMBER: 60/276,947
RNIOR PPLICATION NUMBER: 60/276,947
RNIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6091
TYPE: DNA
ORGANISM: Homo f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/077,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Makielski, Jonathan C
APPLICANT: Ye, Bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 960296.98032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Sodium Channel Alpha Subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 6048 bases
                                                                                                                                                                                                                                                                                             4300 AGGGGG 4305
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48; Conserv
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STRANDEDNESS: double
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72.7%;
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US-10-333-191-1
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                                                                                                                                                                                                                                                                           Sequence 1, Application US/10333191 Publication No. US20030235838A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                    SEQ ID NO 1
                                                                                                            CURRENT APPLICATION NUMBER: US/10/33,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR FILING DATE: 2000-07-20
                                                                                                                                                                                                  APPLICANT: Splawski, Igor
TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in Drug-induced Cardiac
TITLE OF INVENTION: Arrhythmia
FILE REFERENCE: 2323-154-II
                                                                                                                                                                                                                                              APPLICANT: Keating, Mark T. APPLICANT: Splawski, Igor
                                                                                   SOFTWARE: PatentIn version 3.0
                                                                                                  NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
LOCATION: (8167)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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NAME/KEY: modified base
LOCATION: (7477)...(7478)
OTHER INFORMATION: a, t,
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ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: CDS
                         ORGANISM: Homo sapiens
                                          TYPE: DNA
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OTHER INFORMATION: a, t,
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US-09-917-800A-1604

; Sequence 1604, Application US/09917800A
; Patent No. US20020119462A1

; GENERAL INFORMATION:

APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark APPLICANT: Johnson, Kory APPLICANT: Castle, Arthur

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; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1). (8491)
; OTHER INFORMATION: n may be any base
US-10-333-191-3
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US-10-333-191-3
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Best Local :
                                                                                                                  Matches
                                                                                                                                             Query Match
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (151)..(6198)
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/33,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in
TITLE OF INVENTION: Arrhythmia
FILE REFERENCE: 2323-154-II
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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NAME/KEY: misc_feature
LOCATION: (1)...(8491)
OTHER INFORMATION: n may be any base
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                           ACAGAG 90
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APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILIR REFERENCE: 44921-5038-US
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR PPLICANTON NUMBER: US 60/290,029
PRIOR PPLICANTON NUMBER: US 60/290,045
PRIOR PPLICATION NUMBER: US 60/290,045
PRIOR PPLICATION NUMBER: US 60/290,045
PRIOR PILING DATE: 2001-05-13
PRIOR PPLICATION NUMBER: US 60/290,045
PRIOR PILING DATE: 2001-05-14
PRIOR PILING DATE: 2001-05-15
PRIOR PPLICATION NUMBER: US 60/290,356
PRIOR PRIOR PILING DATE: 2001-05-06
PRIOR PPLICATION NUMBER: US 60/290,457
PRIOR PILING DATE: 2001-06-16
PRIOR PPLICATION NUMBER: US 60/290,457
PRIOR PILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
PRIOR PPLICATION NUMBER: US 60/290,459
PRIOR PILING DATE: 2001-06-13
PRIOR PPLICATION NUMBER: US 60/290,459
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PRIOR PPLICATION NUMBER: US 60/290,459
PRIOR PILING DATE: 2001-06-13
PRIOR PPLICATION NUMBER: US 60/290,459
PRIOR PILING DATE: 2001-06-13
PRIOR PPLICATION NUMBER: US 60/290,459
PRIOR PPLICATION NUMBER: US 60/290,349
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Gapop 10.0 , Gapext 1.0
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/ Ggn2_6/ptodata/2/pna/USO6_COMB.seq: *
/ Ggn2_6/ptodata/2/pna/USO7_COMB.seq: *
/ Ggn2_6/ptodata/2/pna/USO8T_COMB.seq: *
/ Ggn2_6/ptodata/2/pna/USO9T_COMB.seq: 
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gn2-6/ptodata/2/pna/US107A_COMB.seq:*
gn2-6/ptodata/2/pna/US107B_COMB.seq:*
gn2-6/ptodata/2/pna/US6001_COMB.seq:*
gn2-6/ptodata/2/pna/US6001_COMB.seq:*
gn2-6/ptodata/2/pna/US6004_COMB.seq:*
gn2-6/ptodata/2/pna/US6004_COMB.seq:*
gn2-6/ptodata/2/pna/US6005_COMB.seq:*
gn2-6/ptodata/2/pna/US6005_COMB.seq:*
gn2-6/ptodata/2/pna/US6006_COMB.seq:*
gn2-6/ptodata/2/pna/US6006_COMB.seq:*
gn2-6/ptodata/2/pna/US6009_COMB.seq:*
gn2-6/ptodata/2/pna/US6010_COMB.seq:*
gn2-6/ptodata/2/pna/US6010_COMB.seq:*
gn2-6/ptodata/2/pna/US6011_COMB.seq:*
gn2-6/ptodata/2/pna/US6011_COMB.seq:*
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gn2-6/ptodata/2/pna/US6011_COMB.seq:*
gn2-6/ptodata/2/pna/US6015_COMB.seq:*
gn2-6/ptodata/2/pna/US6015_COMB.seq:*
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n2-6/ptodata/2/pna/US6021_COMB.seq:*
n2-6/ptodata/2/pna/US6022_COMB.seq:*
n2-6/ptodata/2/pna/US6023A_COMB.seq:*
n2-6/ptodata/2/pna/US6023A_COMB.seq:*
n2-6/ptodata/2/pna/US6023B_COMB.seq:*
n2-6/ptodata/2/pna/US6026_COMB.seq:*
n2-6/ptodata/2/pna/US6026_COMB.seq:*
n2-6/ptodata/2/pna/US6026_COMB.seq:*
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_6/ptodata/2/pna/US6018_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CURRENT APPLICATION NUMBER: US/09/646,224A;
CURRENT FILING DATE: 2000-09-14;
PRIOR APPLICATION NUMBER: GB 9805793.8;
PRIOR FILING DATE: 1998-03-18;
NUMBER OF SEQ ID NOS: 35;
SOFTWARE: PATENTIN Ver. 2.1;
SEQ ID NO 14;
LENGTH: 244;
TYPE: DNA
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US-09-646-224A-14
US-09-646-224A-14
; Sequence 14, Application US/09646224A
; GENERAL INFORMATION:
                                                                                                                                APPLICANT: Glaxo Wellcome PLC
APPLICANT: Tate, Simon N
APPLICANT: Grose, David T
APPLICANT: Hicks, Caroline A
TITLE OF INVENTION: Ion Channels
FILE REFERENCE: PG3432
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US-60-160-190-415
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US-60-207-214-137
US-60-207-214-1398
US-10-170-235-13985
US-60-453-050-2171
3 US-60-466-412-2171
3 US-60-466-412-94
US-10-664-423-94
US-10-664-423-94
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US-10-664-423-60
US-10-664-603-94
US-10-664-603-94
US-10-664-603-60
US-10-664-603-60
US-10-664-603-7
US-60-213-179-53
US-60-213-177-320
US-60-230-445-37
US-60-230-445-677
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US-60-230-445-678
US-60-233-937-3
US-60-233-937-3
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US-60-173-463-166
US-60-173-463-166
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US-09-634-306B-185132
US-10-027-632-185132
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US-60-196-189-98
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Sequence 98, Appl
Sequence 72, Appl
Sequence 84151, A
Sequence 185132,
Sequence 185132,
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US-60-196-189-98

(US-60-196-189-98)

(Sequence 98, Application US/60196189)

(GENERAL INFORMATION:

APPLICANT: Bonazzi, Vivien

(TITLE OF INVENTION: ISOLATED HUMAN TRANSPORITITLE OF INVENTION: NUCLEIC ACID MOLECULES

(TITLE OF INVENTION: AND USES THEREOF

(FILE REFERENCE: CL000441

(CURRENT APPLICATION NUMBER: US/60/196,189

(CURRENT FILING DATE: 2000-04-11

(NUMBER OF SEQ ID NOS: 442

(SOFTWARE: FastSEQ for Windows Version 4.0

(SEQ ID NO 98

LENGTH: 576

TYPE: DNA

(ORGANISM: HUMAN)

US-60-196-189-98
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US-09-646-224A-14
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CCTA 413
                                                                                                      CCAGCAGCTGGGGTTCTCTGGCCTTGTTTCCTTTGGAACAAAACACTATGAGATACCACTG
                                                                                                                                                     GTTATGGTCAAGTCAGAGATATCATGACTACATGGACAGTCCAGAACTGGCGTCATAGTT
                                                                                                                                                                                                                               ATTATATATGCAGCTGTTGATTCCACAGAGGTGAGTCAGTGTTCTACCATGTTCTGGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 244; DB 27; 100.0%; Pred. No. 2.2e-63; ... mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                92.8%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                             Score 226.4; DB 75; Length 576; Pred. No. 6.9e-58; 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCODING HUMAN TRANSPORTER PROTEINS
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US-60-466-412-84151

Sequence | 84151, Application US/60466412

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECT
FILE REFERENCE: CL001466

CURRENT | APPLICATION NUMBER: US/60/466,412

CURRENT | FILING DATE: 2003-04-30

NUMBER OF SEQ ID NOS: 429241

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 84151

LENGTH: 115159
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; Sequence 72, Application US/60207214
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TITLE OF INVENTION: AND USES THEREOF
; TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/207,214
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 622
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 6925
TYPE: DNA
ORGANISM: HUMAN
US-60-207-214-72
                                                                                                                     ORGANISM: Homo sapiens
PRATURE;
NAME/KEY: misc_feature
LOCATION: (1) . (115159)
OTHER INFORMATION: n = A,7
US-60-466-412-84151
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Matches
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Best Local Similarity 95.5%;
Matches 233; Conservative
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                   ATCAGTATTATTCATGTTT
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NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
AND USES THEREOF
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                   Score 226.4; DB 103; Length 115159;
Pred. No. 4.4e-57;
0; Mismatches 11; Indels 0; Ga
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RESULT 6
US-10-027-632-185132/c
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US-09-634-306B-185132/c
, Sequence 185132, Application US/09634306B
, GENERAL INFORMATION:
, APPLICANT: Wang, David G.
, TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
, TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICNG DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.0%;
Best Local Similarity 95.9%;
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LENGTH: 605
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CURRENT APPLICATION NUMBER: US/09/634,306B
CURRENT FILING DATE: 2002-02-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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TCCTTTGGAACAAAACACTATGAGATACCACTGCCTA 244
                                                                                       CTACATGGACAGTCCAGAACTGGCGTCATAGTTCCAGCAGCTGGGGTTCTCTGCCTTGTT
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Pred. No. 1.3e-50;
0; Mismatches 9;
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Sequence 185132, Application US/10027632 GENERAL INFORMATION:

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Sequence 43, Application US/60160190

GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN

ITITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
ITITLE REPERENCE: CLOOO115
CURRENT APPLICATION NUMBER: US/60/160,190
CURRENT FILLING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 2384
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 278
TYPE: DNA
CRGANISM: HUMAN
US-60-160-190-43
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 Query Match 50.2%;
Best Local Similarity 92.1%;
Matches 129; Conservative
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Best Local :
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TYPE: DNA
ORGANISM: Human
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Score 122.4; DB 72;
Pred. No. 2.6e-26;
O; Mismatches 11;
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Pred. No. 1.3e-50;
0; Mismatches 9; Indels 0;
   Indels
                               Length
                                278;
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Sequence 65, Application US/60169841

GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
ITITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN I
ITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000163
CURRENT APPLICATION NUMBER: US/60/169,841
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 2910
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 278
                                                                               ; SEQ ID NO 415
; LENGTH: 460
; TYPE: DNA
; ORGANISM: HUMAN
US-60-160-190-415
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Query Match
Best Local Similarity
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US-60-169-841-65/c
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000115
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CURRENT FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 2384
SOPTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Human
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                 Conservative
                               20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 122.4; DB 72;
Pred. No. 2.6e-26;
0; Mismatches 11;
                 Score 50.2; DB 72;
Pred. No. 0.0003;
0; Mismatches 18;
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                                                Length 460;
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                    Indels
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SEQUENCE 138, Application US/60207214
GENERAL INFORMATION: Beasley, Ellen
TITLE OF INVENTION: USOLATED HUMAN TRANSPORTITIE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00581
CURRENT APPLICATION NUMBER: US/60/207,214
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 622
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 138
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US-60-207-214-137
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GENERAL INFORMATION:
APPLICANT: Beabley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN :
TITLE OF INVENTION: NUCLEIC ACID MOI
TITLE OF INVENTION: AND USES THEREOI
FILE REFERENCE: CL000581
                                                                                                                                                  Best
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Best Local Similarity
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                                                                                                                                                                 Query Match
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CURRENT FILING DATE: 2000-5-26
NUMBER OF SEQ ID NOS: 625
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                  ORGANISM: HUMAN
60-207-214-138
                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTCCACAGAGGTGAGTC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGAGGTGAGTC 97
                                                                CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOLATED HUMAN TRANSPORTER PROTEINS NUCLEIC ACID MOLECULES ENCODING HUMAND USES THEREOF
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79.5%;
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79.5%;
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                                                                                                                              Score 49; DB 76; Length 4740; Pred. No. 0.0016; Indels
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Pred. No. 0.0016;
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US-10-170-235-13985
Sequence 2171, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2171, Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 13985
LENGTH: 5080
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TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
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TYPE: DNA
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Similarity 69.1%;
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Pred. No. 0.0016;
0; Mismatches 30;
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Pred. No.
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0.0016;
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RESULT 15

US-60-466-412-2171
; Sequence 2171, Application US/60466412
; Sequence 2171, Michele
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2171
; LENGTH: 5080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-466-412-2171
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2171
; LENGTH: 5080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-2171
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                                                                                                                       3973 ATGTCAAGGTCTCGTGTTCGACATAGTCACAAGCCAG 4009
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Match Length
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1: /cgn2_6/ptodata/2/pna/PcT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-60-548-091-5511

US-60-548-091-521

PCT-US03-32805-1

PCT-US03-32805-1

PCT-US03-32805-1

PCT-US03-34801-1

US-10-796-280-12297

US-10-796-280-12297

US-10-797-701-21297

US-10-767-471-10865

US-10-797-543-12243

US-10-796-280-1253

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                   Sequence 266, App
Sequence 8171, Ap
Sequence 5535, Ap
Sequence 5580, Ap
Sequence 5581, Ap
Sequence 268, Appl
Sequence 12574, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 95, Appl
Sequence 21297, A
Sequence 21297, A
Sequence 12496, A
Sequence 11246, A
Sequence 1943, A
Sequence 1943, A
Sequence 1413, Ap
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Sequence 5675, Ap
Sequence 5, Appli
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27.8	27.8	28	28	28.2	28.2	28.2	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.6	28.8	29
11.4	11.4	11.5	11.5	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.7	11.8	11.9
15205	201	172943	40000	123504	46917	5091	1184710	230097	154875	44848	44848	41973	41973	39320	28786	327636	403	444922
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US-10-100-683-13164	US-10-796-280-44126	US-10-796-280-12198	US-10-767-471-10914	US-10-767-471-10665	US-10-100-683-12022	US-10-100-683-13029	US-10-796-280-12394	US-10-796-280-12390	US-10-765-790-107	US-10-785-116-42	US-10-781-758-42	US-10-796-280-12385	US-10-767-471-10733	US-10-767-471-10781	US-10-767-471-10789	US-60-550-051-2994	US-09-796-692B-4717	US-60-550-051-3005
Sequence 1	Sequence 4	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence	Sequence 1	Sequence 1	Sequence 4	Sequence 4	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 2	Sequence 4	Sequence 3
3164, A	4126, A	.2198, A	.0914, A	.0665, A	2022, A	.3029, A	12394, A	2390, A	07, App	2, Appl	2, Appl	.2385, A	.0733, A	.0781, A	.0789, A	1994, Ap	717, Ap	3005, Ap
	6 US-10-100-683-13164 Sequence	6 US-10-796-280-44126 Sequence 6 US-10-100-683-13164 Sequence	6 US-10-796-280-12198 Sequence 6 US-10-796-280-44126 Sequence 6 US-10-100-683-13164 Sequence	6 US-10-767-471-10914 Sequence 6 US-10-796-280-12198 Sequence 6 US-10-796-280-44126 Sequence 6 US-10-100-683-13164 Sequence	6 US-10-767-471-10665 Sequence 6 US-10-767-471-10914 Sequence 6 US-10-796-280-12198 Sequence 6 US-10-796-280-44126 Sequence 6 US-10-100-683-13164 Sequence	28.2 11.6 46917 6 US-10-100-683-12022 Sequence 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 28 11.5 40000 6 US-10-767-471-10914 Sequence 28 11.5 172943 6 US-10-796-280-12198 Sequence 27.8 11.4 201 6 US-10-796-280-44126 Sequence 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	39 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 40 28.2 11.6 46917 6 US-10-100-683-12022 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28 11.5 40000 6 US-10-767-471-10914 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 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US-10-796-280-12394 Sequence 39 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 40 28.2 11.6 46917 6 US-10-100-683-13029 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28.2 11.5 13504 6 US-10-767-471-10914 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 15205 6 US-10-796-280-13164 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	35 28.4 11.6 44848 6 US-10-785-116-42 Sequence 36 28.4 11.6 154875 6 US-10-785-790-107 37 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 38 28.4 11.6 230097 6 US-10-796-280-12394 Sequence 39 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 40 28.2 11.6 46917 6 US-10-100-683-12022 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28 11.5 172943 6 US-10-767-471-1994 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 201 6 US-10-796-280-13196 Sequence 45 27.8 11.4 15205 6 US-10-796-280-13164 Sequence	34 28.4 11.6 44848 6 US-10-781-758-42 35 28.4 11.6 44848 6 US-10-781-16-42 36 28.4 11.6 154875 6 US-10-785-790-107 37 28.4 11.6 154875 6 US-10-765-790-107 38 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 39 28.2 11.6 230097 6 US-10-796-280-12394 Sequence 40 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 41 28.2 11.6 46917 6 US-10-100-683-12022 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28 11.5 123504 6 US-10-767-471-10914 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 201 6 US-10-796-280-44126 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	33 28.4 11.6 41973 6 US-10-796-280-12385 Sequence 34 28.4 11.6 44848 6 US-10-781-758-42 Sequence 35 28.4 11.6 44848 6 US-10-785-116-42 Sequence 36 28.4 11.6 154875 6 US-10-765-790-107 37 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 38 28.4 11.6 1184710 6 US-10-796-280-12394 Sequence 39 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 40 28.2 11.6 46917 6 US-10-100-683-13029 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28 11.5 40000 6 US-10-796-280-12194 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 25205 6 US-10-796-280-12198 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	32 28.4 11.6 41973 6 US-10-767-471-10733 Sequence 34 28.4 11.6 41973 6 US-10-796-280-12385 Sequence 34 28.4 11.6 41848 6 US-10-781-758-42 35 28.4 11.6 44848 6 US-10-781-758-42 36 28.4 11.6 44848 6 US-10-785-116-42 Sequence 37 28.4 11.6 230997 6 US-10-795-280-12390 Sequence 38 28.4 11.6 230997 6 US-10-796-280-12394 Sequence 39 28.4 11.6 230997 6 US-10-100-683-12022 Sequence 40 28.2 11.6 46917 6 US-10-100-683-12022 Sequence 41 28.2 11.6 46917 6 US-10-765-280-12394 Sequence 42 28.1 1.5 172943 6 US-10-767-471-10665 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 15205 6 US-10-796-280-13164 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	31 28.4 11.6 39320 6 US-10-767-471-10781 Sequence 32 28.4 11.6 41973 6 US-10-767-471-10731 Sequence 33 28.4 11.6 41973 6 US-10-796-280-13385 Sequence 34 28.4 11.6 44848 6 US-10-781-758-42 Sequence 35 28.4 11.6 44848 6 US-10-781-758-42 Sequence 36 28.4 11.6 154875 6 US-10-785-790-107 Sequence 37 28.4 11.6 154875 6 US-10-765-790-107 Sequence 38 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 39 28.4 11.6 230097 6 US-10-796-280-12394 Sequence 39 28.2 11.6 5091 6 US-10-100-683-13022 Sequence 40 28.2 11.6 46917 6 US-10-100-683-13022 Sequence 41 28.2 11.6 123504 6 US-10-767-471-10665 Sequence 42 28 11.5 172943 6 US-10-767-471-10965 Sequence 43 28 11.5 172943 6 US-10-796-280-12198 Sequence 44 27.8 11.4 15205 6 US-10-796-280-44126 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence	30 28.4 11.6 28786 6 US-10-767-471-10789 Sequence 32 28.4 11.6 39320 6 US-10-767-471-10781 Sequence 28.4 11.6 41973 6 US-10-767-471-10733 Sequence 28.4 11.6 41973 6 US-10-796-280-12385 Sequence 34 28.4 11.6 41848 6 US-10-796-280-12385 Sequence 28.4 11.6 41848 6 US-10-781-758-42 Sequence 28.4 11.6 24848 6 US-10-785-716-42 Sequence 38 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 28.4 11.6 230097 6 US-10-796-280-12390 Sequence 28.4 11.6 1184710 6 US-10-796-280-12390 Sequence 28.4 11.6 1184710 6 US-10-0-683-13029 Sequence 28.2 11.6 5091 6 US-10-100-683-13029 Sequence 41 28.2 11.6 123504 6 US-10-706-280-12390 Sequence 28.2 11.6 23504 6 US-10-767-471-10665 Sequence 28.2 11.5 40000 6 US-10-767-471-10914 Sequence 42 28.1 1.5 172943 6 US-10-796-280-12198 Sequence 45 27.8 11.4 15205 6 US-10-796-280-13164 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164 Sequence 45 27.8 11.4 15205 6 US-10-100-683-13164	29 28.6 11.7 327636 7 US-60-550-551-2994 Sequence 31 28.4 11.6 28786 6 US-10-767-471-10781 Sequence 28.4 11.6 39320 6 US-10-767-471-10781 Sequence 32.6 4 11.6 41973 6 US-10-767-471-10733 Sequence 32.6 4 11.6 41973 6 US-10-796-280-12385 Sequence 32.6 4 11.6 41848 6 US-10-781-758-42 Sequence 32.6 4 11.6 41848 6 US-10-781-758-42 Sequence 32.6 4 11.6 230997 6 US-10-785-716-42 Sequence 32.6 4 11.6 230997 6 US-10-785-280-12390 Sequence 32.6 4 11.6 230997 6 US-10-796-280-12394 Sequence 33.2 21.6 23091 6 US-10-796-280-12394 Sequence 34.2 21.6 46917 6 US-10-0-683-12022 Sequence 42.2 21.6 46917 6 US-10-768-3-12022 Sequence 42.2 21.5 40000 6 US-10-767-471-10665 Sequence 43.2 28 11.5 172943 6 US-10-796-280-12194 Sequence 44.2 27.8 11.4 15205 6 US-10-796-280-13164 Sequence 45.2 11.6 11.4 15205 6 US-10-796-280-13164 Sequence 45.2 11.6 11.4 15205 6 US-10-796-280-13164 Sequence 45.2 11.6 11.4 15205 6 US-10-100-683-13164 Sequence 45.2 11.6 11.6 11.6 US-10-100-683-13164 Sequence 45.2 11.6 11.6 US-10-100-683-13164 Sequence 45.2 11.6 11.6 US-10-100-683-13164 Sequence 45.2 US	28 28.8 11.8 403 5 US-09-796-69284-717 29 28.6 11.7 327636 7 US-60-550-051-2994 30 28.4 11.6 28786 6 US-10-767-471-10789 31 28.4 11.6 39320 6 US-10-767-471-10781 32 28.4 11.6 41973 6 US-10-767-471-10781 32 28.4 11.6 41973 6 US-10-767-471-10733 32 28.4 11.6 41973 6 US-10-786-280-12385 33 28.4 11.6 44948 6 US-10-785-116-42 34 28.4 11.6 44948 6 US-10-785-116-42 35 28.4 11.6 230997 6 US-10-785-11290 36 28.4 11.6 230997 6 US-10-785-11390 38 28.4 11.6 230997 6 US-10-796-280-12394 39 28.2 11.6 230997 6 US-10-10-683-13022 40 28.2 11.6 46917 6 US-10-100-683-12022 41 28.2 11.6 46917 6 US-10-796-280-12394 42 28 11.5 172943 6 US-10-767-471-10665 43 28 11.5 172943 6 US-10-767-471-10965 44 27.8 11.4 15205 6 US-10-796-280-13198 45 27.8 11.4 15205 6 US-10-796-280-13164 48 27.8 11.4 15205 6 US-10-796-280-13164 49 28 28 11.4 15205 6 US-10-796-280-13164 40 28 28 11.4 15205 6 US-10-796-280-13164 41 28 28 11.5 172943 6 US-10-767-471-10665 42 28 11.4 15205 6 US-10-796-280-13164 43 28 11.4 15205 6 US-10-796-280-13164 44 27.8 11.4 15205 6 US-10-796-280-13164

## ALIGNMENTS

RESULT 1 US-60-548-091-19213

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CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19213
ELENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-60-548-091-19213
                                                                                                                               RESULT 2
US-60-548-091-5675
(Sequence 5675, Application US/60548091
; Sequence 5675, Application US/60548091
; GENERAL INFORMATION:
GENERAL OF INVENTION:
STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 24433
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19213, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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                                                                                                                 SEQ ID NO 5675
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                     LENGTH: 100374
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TCGTTTATGCAGCTGTTGATTCCACAGAGGTGAGT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%;
Similarity 66.3%;
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Pred. No. 1.6e-05;
1; Mismatches 31; Indels
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A,T,C or G,

or insertion/deletion polymorphism (see Tables

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; LOCATION: (1)...(100374); OTHER INFORMATION: n = A US-60-548-091-5675
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APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
APPLICANT: Louis POON
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS ANI
FILE REFERENCE: 117-492 / N.86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
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                                                                                                                                                                                               Sequence 1, Application US/10487337 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REFERENCE: 117-492 / N.86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR PTILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR PILING DATE: 2001-08-20
NUMBER: OF SEQ ID NOS: 55
NUMBER: OF SEQ ID NOS: 55
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APPLICANT: Mark BAKER
APPLICANT: Louis POON
APPLICANT: John Nichol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (1)..(5874)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5874
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.3%; es 63; Conservation
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Pred. No. 0.00018;
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                                                                              AND MODULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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; ORGANISM: Homo sapiens
US-60-548-091-267
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                                                                                                                                                                                                                                             RESULT 6
US-60-548-091-266
                                                                         ; Sequence 266, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01506
; CURRENT APPLICATION NUMBER: US/60/548,091
; CURRENT FILING DATE: 2004-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
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NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 4855
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ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: CDS
LOCATION: (204)..(6074)
OTHER INFORMATION:
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PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 24433 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 4852
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                                                                                                                                                                                                                                                                                                                           3186 AGGGGG 3191
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Similarity 74.3%;
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Pred. No. 0.022;
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US-60-545-213-8171
; Sequence 8171, Application US/60545213
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-60-545-213-3899
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: William Martin
APPLICANTON UNMER: US/60/545,213
CURRENT APPLICATION UNMER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
SOFTWARE: Patentin version 3.2
SEQ ID NO 3899
LENGTH: 600
                                                                                                                                                                                                                APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 8111
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Best Local Similarity 77.2%;
Matches 44; Conservative
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Best Local Similarity
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                                                                                                            Query Match
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60-545-213-8171
                                                                                                                                                                                 TYPE: DNA
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ORGANISM: Homo sapiens
                                                             y match
Local Similarity 77.2%;
108 44; Conservative
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GCCACATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTG 360
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                                                                   Score 36.2; DB Pred. No. 0.02; 0; Mismatches
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RESULT 11
US-60-548-091-268
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US-60-548-091-5535
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5580
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5535
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILLING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FRASSEQ for Windows Version 4.0
SEQ ID NO 268
LENGTH: 4855
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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78.2%;
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71.2%;
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Pred. No. 0.01
0; Mismatches
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TYPE: DNA

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; Sequence 12574, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
; TITLE OF INVENTION: STENOSIS, METHODS OF DE
; FILE REFERENCE: CL001510
; CURRENT APPLICATION UMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
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US-60-548-091-5511
; Sequence 5511, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH;
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001506
; FILE REFERENCE: CL001506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-60-548-091-268
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US-10-796-280-12574
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; ORGANISM: Homo sapiens
US-60-548-091-5511
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Best Local Similarity 74.0
44; Conservative
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Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12574
LENGTH: 156796
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5511
LENGTH: 201
                                                                                                                                             Matches
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
                                                                                                                                                            Match 14.3%;
Local Similarity 57.3%;
                                                                     97839
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                                 79 GATTCCACAGAGGTGAGTCAGTGTTCTACCATGTTCGGCAGTGTTATGGT 128
                                                                                                                                         63;
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                                                                                                   GATCCTAGAGTGCAGTATTTGGGATATACTATGAAAGTGTTTGCTAAGGT 97948
                                                                     Conservative
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STENOSIS, METHODS OF DETECTION AND U
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Pred. No. 0.073; 
0; Mismatches 19; Indels 0
                                                                                                                                         Score 34.8; DB Pred. No. 0.53; 0; Mismatches
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Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                            DB 6;
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RESULT 14
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Susceptibility Gene for Myocardial TITLE OF INVENTION: Infarction FILE REFERENCE: 2345.2048002 CURRENT APPLICATION NUMBER: PCT/US03/32805 CURRENT FILING DATE: 2003-10-16 PRIOR APPLICATION NUMBER: 60/419,432 PRIOR APPLICATION NUMBER: 60/419,432 PRIOR FILING DATE: 2002-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 535
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (70677)...(70776)
OTHER INFORMATION: n = A,T,
                                                              FEATURE:

NAME/KEY: misc_feature
LOCATION: (350504)...(350603)

OTHER_INFORMATION: n = A,T,C
                                                                                                                                                      FEATURE: misc feature
NAME/KEY: misc feature
LOCATION: (345190)...(345289)
OTHER INFORMATION: n = A,T,C
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LOCATION: (341698)...(341698)
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LOCATION: (332849)...(332948)
OTHER INFORMATION: n = A,T,C
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LOCATION: (327555)...(327654)
OTHER INFORMATION: n = A,T,C
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LOCATION: (279545)...(279644)
OTHER INFORMATION: n = A,T,C or
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LOCATION: (272544)...(272643)
OTHER INFORMATION: n = A,T,C
FEATURE:
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LOCATION: (269991)...(270091)
OTHER_INFORMATION: n = A,T,C
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LOCATION: 248521
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LOCATION: (154988)...(155087)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                             OTHER INFORMATION: n = A, T, C
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OTHER INFORMATION: n = A, T, C
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NAME/KEY: misc_feature
LOCATION: (391524)...(391623)
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Gulcher, Jeffrey R.
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APPLICANT: GECODE genetics ehf.
APPLICANT: Reynisdotti; Inga
APPLICANT: Reynisdotti; Inga
APPLICANT: Gulcher, Jeffrey R.
APPLICANT: Grant, Struan F.
APPLICANT: Thorleifsson, Gudmar
TITLE OF INVENTION: Human Type II Diabetes Gene - Slit-3
TITLE OF INVENTION: Located on Chromosome 5q35
FILE REFERENCE: 2345.2046002
CURRENT APPLICATION NUMBER: PCT/US03/34801
CURRENT APPLICATION NUMBER: 60/423,541
PRIOR APPLICATION NUMBER: 60/423,541
PRIOR APPLICATION NUMBER: 60/423,541
PRIOR FILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 236
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO | 1
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Search completed: March 23, 2004, 04:50:26
Job time : 328.212 secs
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TYPE: DNA
ORGANISM: homo sapiens
PCT-US03-34801-1
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PCT-US03-34801-1
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Best Local Similarity
Matches |80; Conserv
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                                                                                                                                                                                                      78253 GCTAACCTGCATTCATGTAATGGCTCTGCATATACCAACACTGCATGAAAGGACTGGATC 78312
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                                                                                                                                                                                                                                                                                                            GGGCTGGGGAGATTTCACCATGGCTCCTGGTGCTTCTCTCTGGGTGACAATGGCTGAAGT 78252
                                                                                                                                           TGGCGTCATAGTTCCAGCAGCTGGGGTTCTCTGCCTTGTTT 208
                                                                                                      TGGAGACATTCTTCCTAAAGCAAAAATTCTGCATTATGTTT 78353
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ilarity 49.7%;
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ALIGNMENTS

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CIN CE215453.1 GI:35371122
SS CANIS familiaris (dog)
CIN CANIS FAMILIARIS (CANNIVOTA; FISSIPEDIA; CANIDAC, CANIS.
CIN CANIS FAMILIARIS
CIN CANIS (CANNIVOTA; FISSIPEDIA; CANIDAC, CANIS.
CIN CANIS (CANIDAC, CANIDAC, CANIDAC, CANIS.)
CIN CHARLES E.F., Baffna, V., Halpern, A.L., Levy, S., Remington, K., Venter, J.C.
The dog genome: survey sequencing and comparative analysis
CONTROL SCIENCE 301 (5641), 1898-1903 (2003)
CONTROL XIKNESS EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0200
Email: ekirknessetigr.org

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REFERENCE
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AUTHORS
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AY404475
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JOURNAL
                                                                                    Query Match
Best Local Similarity
Matches 67; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4614)
2 (lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 4614)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens SCN11A gene, VIRTUAL genomic survey second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class:
                                                                                                                                                                                                                                                                                                                                                        Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY404475.1 GI:39760452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
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Direct Submission
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                    GGCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAGAACAA 3506
                                        GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAGGTGAG
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ilarity 69.1%;
Conservative
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/mol_type="genomic DNA"
/strain="standard Poodle"
/db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries we peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shotgun
                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                         'locus_tag="HCM1903"
                                                                                                                                                                                           'gene="SCN11A"
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                                                                                    Score 49; DB 29;
Pred. No. 0.033;
0; Mismatches 30
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 GTACGCAGCTGTAGATTCTCGTGATGTAAGTGTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TTATGCAGCTGTTGATTCCACAGAGGTGAGTCAGTGTT 103
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoblowi,
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 800)

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 3772)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                    Pan troglodytes SCN11A gene, genomic survey sequence. AY404476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus, Hinxton, Cambridgeshire, CB10 1SA, I humquery@sanger.ac.uk Unpublished This sequence was generated from the SP6 end is part of the Daniokey BAC Library created Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
Danio rerio
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Danio rerio genomic clone
BX238165
                                                       Science 302
                                                                     gene trios
                                                                                                                                                                                                                                Pan troglodytes (chimpanzee)
Pan troglodytes
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                                  14671302
                                                                                          Inferring nonneutral evolution from human-chimp-mouse orthologous
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                  (bases 1 to 3772)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
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                                                     (5652), 1960-1963 (2003)
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DKEY-286P24,
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                                                                                                                                                                Kejariwal, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0

Plate: 0167 row: K column: 19

Seq primer: CGTTGTAAAACGACGGCCAGT

Class: plasmid ends
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                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Ress
                                                                                                                                                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ861116

256 bp DNA line
2m0167K19F Mouse 10kb plasmid UUGC1M library Mu
clone UUGC2m0167K19 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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AZ861116.1 GI:13057114
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAACATTTAAGGGCTGGATGGATATTATATATGCAGCTGTTGATTCCACAGAGNNNNNN 3507
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                                                                         quality sequence stop: 256
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pan troglodytes"
|mol_type="genomic DNA"
/mol_type="genomic DNA"
                     /organism="Mus musculus"
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Pred. No. 0.06;
0; Mismatches 115; Indels
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REFERENCE
AUTHORS
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CB608527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574 bp
AMCINUC: NRDG1-00143-D3-A nrdg1 (
nrdg1-00143-d3 5', mRNA sequence
CB608527
                                                                                                                                                                                                                                                                                                                                                                    Amgen EST Program
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                            One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
Plate: 00143 row: d column: 3.
                                                                                                                                                                                                                                                                                                                                             Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 574)
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/tissue type="Dorsal Root Ganglia"
/clone_Tib="nrdg1 (10855)"
/note="Vector: psporti; Site_1: Sall; Site_2: Not1; rat dorsal root ganglia"
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                                                                                                /organism="Rattus norvegicus"
/mol type="mRAN"
/mb xref="taxon:10116"
/clone="nrdg1-00143-d3"
                                                                                                                                                                                                                     Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/db_xref="taxon:10090"
/clone="UUGC2M0167K19"
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KEYWORDS
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DEFINITION
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Best Local Similarity
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Best Local Similarity
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Kremitzki,C., Higginbotham,J., |
Warren,W., Graves T., Mardis E.
Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC295710 1084 bp DNA linear GC295710 1084 bp DNA linear GCH261-146M14_RM1.1 CH261 Gallus gallus genomic clone
CB534807 519 bp mRNA 768167 MARC 6BOV Bos taurus cDNA 3', mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: RM1 TACGACTCACTATAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Richard K. Wilson
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                                                                                               GCAATGTAAGT 675
                                                                                                                            CAGAGGTGAGT 96
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                                                                                                                                                            TCTGTTTATAGGCTACATTTAAAGGATGGATGGATATCATGTATGCAGCTGTGGATTCTC 664
                                                                                                                                                                                        TTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCA 85
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ilarity 74.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence start: 20 quality sequence stop: 745.
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                    /cell_line="UCD001, inbred 256"
/clone lib="CH261"
/clone lib="CH261"
/note="Vector: pTRRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-146M14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
/mol type="genomic name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     sex="female"
                                                                                                                                                                                                                                         16.6%;
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Pred. No. 3.7;
0; Mismatches
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                                                                                                                                                                                                                                         Score 40.6; I
Pred. No. 4.9;
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  and Wilson,R.
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 mRNA sequence.
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E CH261-146M14,
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VERSION
KEYWORDS
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RESULT 9
BF347024
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 TGATTCCACAGAGGTGA
                                                                                                                                                                                                                                                                                                               689 bp
602021819F1 NCI_CGAP_Brn67 Homo
5', mRNA sequence.
BF347024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB534807
CB534807.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                           1 (bases 1 to 689) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified v cross match v0.990329.

Plate: LAM8018 row: M column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 519)
Smith, T.P.L., Rober
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                  BF347024.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
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                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/inotary_made_with_RNA_pooled_from_multiple_tissues
including_liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                  GI:11294619
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                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
Incyte Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40.2; DB Pred. No. 6.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                          mRNA linear EST 22-NOV-2
sapiens cDNA clone IMAGE:4157189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519;
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Sequencing by:

75

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ACCESSION
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CB761310
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Best Local S
Matches 54
             Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
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http://image.llnl.gov
Plate: LLAM9431 row: f column:
High quality sequence start: 3
High quality sequence stop: 654.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB761310
430 bp mRNA linear
AMGNNUC:NRHY4-00021-H1-A W Rat hypothalamus (10464)
norvegicus cDNA clone nrhy4-00021-h1 5', mRNA sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB761310.1 GI:29849701
EST.
                                                                                                                                                                                                                                                   Plate:
                                                                                                                                                                                                                                                     One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
Plate: 00021 row: h column: 1.
                                                                                                                                                                                                                                                                                                                 Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 430)
Amgen EST Program
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB761310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 70.1
54; Conservative
             Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can ound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATTCCACAGAGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="nawn"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGB:4157189"
/tissue_type="anaplastic oligodendroglioma with lp/19q
/tissue_type="anaplastic oligodendroglioma with lp/19q
                                                                                    /db_xref="taxon:10116"
/clone="nrhy4-00021-hl"
/clone_lib="W Rat hypothalamus (10464)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; W
hypothalamus adult female Wistar rat avg. Insert size
kb fraction 6 and 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/clone_Tib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
onl_type="mRNA"
                                                                                                                                                                                    organism="Rattus norvegicus"
|mol_type="mRNA"
                                                                                                                                                                                                                                   ocation/Qualifiers
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                          16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
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             0,
             Score 40; DB 14; Length 430; Pred. No. 7.5; Indels
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Sciurognathi;
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thi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                                                                                                                                                                                    91320-1799, USA
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Rattus
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             0
             Gaps
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CB720975
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BU116614
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JOURNAL
MEDLINE
PUBMED
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Best Local (
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                      14 GGCAACCTTCAAAGGCTGGATGGACATAATGTATGCAGCTGTTGATTCCGGAGAGATCA 72
                                                                                                                                                                                                                                                                                                                                                                                                  36 GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAGGTGA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 833)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W.; Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs (Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                  sequence.
BU116614
                                                                                                                                                                                                                                                                 BU116614 833
603139753F1 CSEQCHL15 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMGNNUC:NRDG1-00043-D7-A nrdg1 (; nrdg1-00043-d7 5', mRNA sequence CB720975
                                                                                                                                                                   Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 805 447-4881
Plate: 00043 row: d column:
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                                                                                                                                                                                 Gallus gallus (chicken)
                                                                                                                                                                                                                  BU116614.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB720975.1 GI:29778117
                   22335534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dorsal root ganglia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdg1-00043-d7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
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                                                                                                                                                                                                                    GI:25323565
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.2; DI
Pred. No. 21;
0; Mismatches
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                                                                                                                                                                                                                                                                 bp m
gallus
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         띪
                                                                                                                                                                                                                                                                     mRNA line
                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                     linear EST 25-NOV-2002
one ChEST129j14 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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Contact:

Simon Hubbard

12445392

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ACCESSION
VERSION
KEYWORDS
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                                           FEATURES
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Matches 44; Conserv
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                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University (UMIST)
                                                           Email: gwaldbieser@ars.usda.gov
Single pass sequencing. Bases called with Phred v0.000925.c. Low
quality bases and vector trimmed with Lucy v1.16.
Plate: Br1 10 row: C column: 1
Seq primer: M13 Reverse.
                                                                                                                                                                                                                Catfish Genetics Research Unit USDA-Agricultural Research Service
                                                                                                                                                                                                                                                                                                       (Ictalurus punctatus)
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                  Nonneman,D.J. and Waldbieser,G.C. Characterization of a brain cDNA library from adult channel catfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IpCGBr1_10_C01_21 Ictalurus punctatus Brain1 primary library
Ictalurus punctatus cDNA clone IpCGBr1_10_C01_21_06Mar00_006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences University of Manchester Institute
                                                                                                                                                                 Tel: 662 686 3593
Fax: 662 686 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM494034.1 GI:18645215
                                                                                                                                                                                                                                                                                       Contact: Waldbieser GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ctalurus punctatus (channel catfish)
                                                                                                                                                                                                                                                                                                                                                                                             ctaluridae; Ictalurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CSEQCHL15"
//clone_lib="CSEQCHL15"
//note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
RCORI; Site_2: Not1; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggccgcgtgcagcccggatccgaaaaaaaag]
[5'aattctttttttcggatccggggctgcacgc]"
                                        Location/Qualifiers
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/organism="Ictalurus punctatus"
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ORGANISM
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KEYWORDS
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BQ946179
LOCUS
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                                                                                                               Best Local Similarity
Matches 48; Conserv
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 GGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCCACAGAGGT 92
85
                                                                         25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
1 (Dases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENCOURT_8926526 NIH_MGC_94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ946179.1 GI:22361657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence.
BQ946179
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45; Conservative
ACAGAG 90
                                   CTTCTTCAAGTGGCAACCTTCAAAGGCTGGATGGACATCATGTATGCAGCTGTAGATTCC
                                                                         CTTTTTTTGCAGGCACAATTTAAGGGCTGGATGGATATCGTTTATGCAGCTGTTGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 596.
Location/Qualifiers
                                                                                                                 Conservative
                                                                                                                                                                                                       /mol type="mRNA"

/db xref="taxon:10090"
/clone="MRAGE:6469275"
/tissue_type="retina"
/tab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="NIH MGC 94"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/clone="IpCGBr1 10 C01 21_06Mar00_006"
/sex="female and male"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Ictalurus punctatus Brain1 primary library"
/note="Organ: brain; Vector: pSport1; Site_1: Sal 1;
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/strain="USDA103"
                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"/
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78.9%;
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72.7%;
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                                                                                                                                   Score 37.2;
Pred. No. 36;
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Pred. No. 2
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Mus musculus cDNA clone
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Tsurumi-ku, Yokohama

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ACCESSION
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AK083220
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                                                                                                                                              Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiraoka, C., Hiraoka, T., Hiraoka, T., Hiraoka, T., Hiraoka, T., Hiraoka, T., Hiraoka, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Sasito, R., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Shinagawa, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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20499374
11042159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4675)
Nature 1 to 4675
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN Genome Exploration Research
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further
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URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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SUMMARIES

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KEYWORDS SOURCE ORGANISM RESULT 1 AX017231 LOCUS REFERENCE DEFINITION ACCESSION VERSION AUTHORS TITLE JOURNAL AX017231 Sequence 15 AX017231 AX017231.1 Homo Tate, S.N., Grose, D.T. and Hick, C.A. Mammalian sodium channel proteins Patent: WO 9947670-A 15 23-SEP-1999; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. sapiens (human) sapiens 15 GI:10042151 from Patent 409 bp WO9947670. DNA linear PAT 07-SEP-2000

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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E 1 (bases 1 to 409)

S Grose,D.T., Hick,C.A. and Tate,S.N.

Mammalian sodium channel protein

Patent: JP 2002508941-A 14 26-MAR-2002;

GLAXO GROUP LTD

OS Homo sapiens (human)

PN JP 2002508941-A/14

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PF 18-MAR-1999 JP 2000536853
PF 18-MAR-1999 GB 9805793.8
PR 18-MAR-1998 GB 9805793.8
PR 18-MAR-1998 GB 9805793.8
PI DAVID THOMAS GROSE, CAROLLNE ANNE HICK, SIMON NICHOLAS TATE C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, ICLAN15/09, A61P17/04, A61
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  SOEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian sodium channel
                                                                                                                                      C12N1/19, C12N1/21, C12N5/10, C12Q1/02, G01N33/15, G01N33/50, G01N33/
                                                                                                                                                                                                 C12N1/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD138453.1 GI:23233398
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                          Key
                                                       Mammalian sodium
                                                                                  C12N15/00, C12N5/00
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                      and nawy---,
Direct Submission
Submitted (28-JUN-2002) Genome
Submitted (28-JUN-2002) Genome
Submitted (28-JUN-2002) Genome
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AC116038.3
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Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 167476)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Buckley, D., Kibukawa, M.,
                                                                                                                                                              Kaul, R.K., Olson, M.V., Zhou, Y., Saenphimmachak, C., Phelps, K.A., and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 167476)
Kaul, R.K., Olson, M.V., Raymond, C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ebkaryota; Metazoa; Chordata; Cl
Mammalia; Eutheria; Primates; Cc
Mammalia; Eutheria; Primates; Cc
1 (bases 1 to 167476)
Kaul, R.K., Olson, M.V., Zhou, Y.,
Saenphimmachak, C., Buckley, D., F
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                                                                                                                                                                                                                                                   Box 352145, Seattle, W
3 (bases 1 to 167476)
                                                                                                                                                                                                                                                                                                                Submitted (23-MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC116038 167476 bp
Homo sapiens chromosome 3 clone
                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Primates;
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                                                                                       Center,
USA
                                                                                                                                                                                                                                                                                         Center,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James, R.A.,
Kibukawa, M.,
                                                                                                                                                                                                 James,R.A.,
Buckley,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP11-134J21,
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DNA

linear

inear PRI 07-OCT-2003 complete sequence.

Haugen, E University

of Washington,

Rouse, G., Wu, Z., Raymond, C. and

University

of Washington

Rouse, G., Wu, Z., Raymond, C. and

Rouse, G., Kibukawa, I

, M. Wu,

, Z., Raymond, C.

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GAAACACCTTGGTCTTCTAGATAAGGTAGTTAGAATGCTTATATTTTTTCTCCAGTAATTG
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                    GGTTGTCTTGATTTGGTAATTGTATCTCTGTCCTCCAAAGAAGAAGAATCC 409
                                                                                                                                                                                                                                                                                                                                                                                         GAAACACCTTGGTCTTCTAGATAAGGTAGTTAGAATGCTTATATTTTTCTCCAGTAATTG
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                                                                                         TCTCTTCATTGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAAGATAAGTATCTG
                                                                                                                     TCTCTTCATTGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTG 360
                                                                                                                                                                                          ATTCACTCGGTTACATTTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAA
                                                                                                                                                                                                                   ATTCACTCGGTTACATTTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAA 300
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Pred. No. 1.9e-83;
; Mismatches 0;
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		TITLE JOURNAL COMMENT
SeqDerMap F	Center: University of Wash. Center: University of Wash. Center Code: UWGC Web site: http://www.genome Contact: uwgchtgs@u.washing. Center project name: RP11-13. Center clone name: RP11-13. Center clone name: RP11-13. Center clone name: RP11-13. Center clone name: RP11-13. Center project name: RP11-13. Center project name: RP11-13. Center clone name: RP11-13. Center clone quality: 167467   Consensus quality: 167476   Insert size: 167476; sum-ol Quality coverage: 18.9x in Center size: 167476; sum-ol Quality coverage: 18.9x in Center size: 167476; sum-ol Quality coverage: 18.9x in Center size: 167476; sum-ol Quality levels above 40 are site sentry has been annotated estimates computed by the Phra Quality levels above 40 are si error in 10,000 bp. Base-by not generally visible from the but are available as part of covered destimates chemistry or covered quality = 30; an attempt was problems, such as compressions sproblems, such as compressions of fingerprinting. Comparison of fingerprinting. Comparison of fragments with sequence-prediction of the electronically-digested sprometry are not resolved in the finger in the table. There are no side between the experimental and if fragments are separated by data fragments are separated by	Haugen, E.D. Direct Submission Submitted (07-OCT Box 352145, Seatt On Oct 7, 2003 th
FngrPrnt 	Center: Universit. Center: Universit. Center: Universit. Center Code: UwgCt Center Code: UwgCt Center clone name Center project Center clone name Center clone name Center project Consensus quality Consensus project Consensus quality Consens	mission (07-OCT-2003) Seattle, WA
SeqDerMap F	Himmige dod amnage to be co, in this and the control of the contro	Genon 98199
PngrPrnt  2741 6514 <800 <800 2741 4878	ngton Genome C .washington.ed ton.edu ion 221 (bc0780) 8 100% of reads 7; 45% of reads 7; 45% of reads 100% of reads gove; 55% of resion 0.990319 ases at least ases at least ases at least contigs Q20 bases; sum Q20 b	ter, Univ
SeqDerMap	ngton Genome Centerwashington.edu tion 100% of reads 11 (bc0780) 121 (bc0780) 133 of reads 11 ye; 55% of reads 12 ye; 55% of reads 12 ye; 55% of reads 13 ye; 55% of reads 13 ye; 55% of reads 14 least Q40 15 sees at least Q40 15 sees at least Q20 15 contigs 16 yer reads 17 (Afther the contigs 18 (Afther the contigs 18 (Afther the contigs 19 yeasembly program, 19 pected to have less than 19 pected to have less than 10 pected to have less than 10 pected to have less than 11 pected to have less than 12 pected to have less than 13 pected to have less than 14 pected to have less than 15 pected to have less than 16 pected to have less than 17 pected to have less than 18 pected in sequence 18 pected to have less than 18 pected to resolve all sequencing 18 pected or sequence than one M13 18 confirmed by restriction digest 18 pected the pected digest 18 pected the pected of both insert and 18 pected tragments is given below. 19 print and hence do not appear 10 pected to the values. Uniquely ordered 10 pected the dilnes. 10 pected to the values. 10 pected to the values. 10 pected to the pected the dilnes. 10 pected to the pected the dilnes. 10 pected to the pected the dilnes. 10 pected to the pected the pected to the pected the pected to the pected the pect	ne Center, University of Wash 5, USA version replaced gi:21622736
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<800 7213 6159 <800 8629 <800 3718 3718	<pre>&lt;800 6560 4771 3447 &lt;800 3091 &lt;800 5088 6560 9211 &lt;800 9211 &lt;800 9211 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800 1370 6800</pre>	3447 <800 <800
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	TITLE Mus musculus chromosome 9, clone RP24-409K22
- ,	Eukaryota; Metazoa; Ch Mammalia; Eutheria; Ro 1 (bases 1 c 241289)
	AC124662.5 GI:38490569 HTG; HTGS: PHASE1; HTGS: FULLTOP; HTGS_ACTIVEFIN. Mus musculus (house mouse) M Mus musculus
	IN PROGRESS ***, 11 unordered pieces. AC124662
	RESULT 4 AC124662
-	Db 101208 GGGTTGTCTTGATTTGGTAATTTTATCTCTGTCCTCCAAA 101169
	360 GGGTTGTCTTGATTTGGTAATTGTATCTCTGTCCCAAA
COMMENT	101268 ATCTCTTCATTGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCT
JOURNAL	
	OY 241 ATTCACTCGGTTACATTT-CTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGA 299
	QY 181 TTTTTTCTCTTATTAAAAAATTTCTAACAGAACAACAACAGCCAGAGTTTGAGAGCA 240
	GAAACACCTTGGTCTTCTAGATAAGGTAGTTAGAATGCTTATATTTTTCTCCAGTAATTG
	131
	QY 61 AGGCTCCCAACAGGGGCTATGGCTGTTAGGAAGAGGCTATGTAGTCAATGTTGCTGCTAA 120
	QY 1 ATCCACCCAGGCCCCGCCACATGCCATCACTCCAAGCTGAGAGACTGAAAACTGAAAGAC 60
REFERENCE	Query Macch 89.2%; Score 364.8; DB 9; Length 1674/6; Best Local Similarity 97.8%; Pred. No. 1.5e-73; Matches 391; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
TITLE	567 <800
	5401 5397 4788 4629
	1048 1068 4811 4629
	2033 2040 252 <800
	6843 6824 3630 3727
	731 766 1501 1555 4557 4629
	1560 602 <800 1242
	835 822 511 <800 253 <800
-	309 <800 7414 7557 3335 3339
	1565 1560 1229 1188 2731 2744
AUTHORS	8662 8629 3569 3639 6314 6531
JOURNAL	560 <800 4463 4430 344 <800

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

56842: contig of 56842 bp in length

the accession number will

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CE 2 (Dases I to 241289)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Nusbaum, C., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galgan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrim, J., Manthews, C., McCarthy, M., McSwan, P., McKernan, K., Meldrim, J., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Nicol, R., Norbu, C., Retta, R., Rieback, M., Riley, R., Rise, C., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trajilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Nirect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome RL Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (2014), USA (2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2003 this sequence version replaced gi:38153914.
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Submitted (22-NOV-2003) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
Center project name: L26677
Center clone name: 409_K_22
                                                                                                                                                                                                                                                                                                                                                                                             ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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Nucleic acid encoding E
B36123
B36123.1 GI:13022506
JP 1999235186-A/2.
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Primates; C:
1 (bases 1 to 856)
Paul, S.D., Linda, M.F., Rina, K.,
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70.2%;
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6: contig of 39024 bp in length
6: gap of 100 bp
6: contig of 36950 bp in length
6: gap of 100 bp
8: contig of 5672 bp in length
8: gap of 100 bp
2: contig of 18114 bp in length
2: gap of 100 bp
5: contig of 5593 bp in length
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6: gap of 100 bp
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1: gap of 100 bp
2: contig of 16918 bp in length
1: gap of 100 bp
2: contig of 16918 bp in length
2: contig of 16918 bp in length
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Pred. No. 8.6e-23;
D; Mismatches 91
                                                                                                                                        856 bp Dr
sodium channel
                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Douglas, K.R.
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l of nerve tissue.
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             202 ATTTCTAACAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
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                                                                                                                                                l (bases 1 to 3701)
Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels
Patent: US 6573067-A 6 03-JUN-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                           AR340648
Sequence 6 from
AR340648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI PAUL SHATUA DAITORICHI,LINDA MARIE PISH,RINA KEIRU,
DOUGLAS KENESU RAMBERT,
PI LAKSMI SANGEIMUSUWARAN
                                                                                                                                                                                                                             Unknown
                                                                                                                                                                                                                                       Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                                                                                                                                                                                     TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 1999235186-A/2
31-AUG-1999
20-NOV-1998 JP 1998331769
20-NOV-1997 US 60/066225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C12Q1/68,G01N33/53,G01N33/577,G01N33/68//(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,C12N5/00,C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism='Homo sapiens (human)'
                                                                                                           /organism="unknown"
/mol_type="genomic
                                                                                                                                      1. .3701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                  GI:33732380
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                                                             32.9%;
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patent US 6573067.
                                             0;
                                                Score 134.4;
Pred. No. 1.4e
0; Mismatches
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Pred. No. 1.6e-20;
0; Mismatches 16;
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                                                              .4e-20;
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                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                            root ganglia
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VERSION
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BD217793
LOCUS
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HSA417790
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TITLE
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                                                                                                                                                                                                                                                                                     202
               Homo sapiens mRNA for voltage-gated AJ417790
AJ417790.1 GI:22796539
NAVI.9 gene; voltage-gated sodium of Homo sapiene
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Regulation of sodium channel
BD217793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3701)

Hajj,S.D. and Waxman,S.

Regulation of sodium channel in posterior root ganglion

Patent: JP 2002509860-A 3 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BD217793.1 GI:33027563 JP 2002509860-A/3.
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                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                           ATTCCACAGAGAAAGAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTACT
                                                                                                                                                                                                                                                                                  ATTTCTAACAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
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           .9 gene; voltage-gated sapiens (human)
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                          32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                          .370
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                                                                                                                                                                                                                                                                                                             Score 134.4; DB 6;
Pred. No. 1.4e-20;
0; Mismatches 16;
                          sodium channel
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channel
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                                                                  PRI 09-OCT-2002 (NAV1.9 gene).
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ORIGIN

Query Match Best Local Similarity

32.9%;

Score 134.4; DB 9; Pred. No. 1.4e-20;

Length 5419;

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PUBMED
REFERENCE
AUTHORS
TITLE
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Ludwig-Maximillians-Universitaet,
608, 80802 Muenchen, GERMANY
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22272672
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Neurotrophin-evoked depolarization requires the sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                          SYFTPKKRIJENKKRKSFFLEESKKOPPGSSSEDOÇKKPQLIEQTKRISQNISID
SYFTPKKRKIJENKKRKSFFLEESKKOPPGSSSEDOÇKKPQLIEQTKRISQNISID
HFDEHGDPLQRQRALSAVSIITITMKEQEKSQEPCLPCGENLASKYLVWNCCPQMLCV
KKVLKTVMTGFFTELAITICIIINTVELAMEHKMEASFEKMLNIGNILVETSIFIAEM
CLKIIALDPYHYFRERGWIIFDSIVALLSFADVANCVLJQKRSWFPLRSFRVLRVFFKLAK
CKKILADPYHYFRERGWIIFDSIVALLSFADVANCVLJQKRSWFPLRSFRVLRVFFKLAK
SWPTLNTLIKIIGNSVGALGSLTVVLVIVIFIFSVVGMQLFGRSFNSQKSPKLCNPTG
PTVSCLRHWINGDFWASFILVGEMIENMWECMQEANASSSLCVIVFILITVIG
KLVVLNLFIALLNSFSNEERNGNLEGEARKTKVQLALDRFRRAFCFVGHTLEHFCHK
WCRKQNLPQQKEVAGGCAAQSKDIIPLVMEMKRGSETQBELGILITSVPKTLGVHHOWT
WLAPLAEEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKFTSQRVQSVEIDMESED
EPHLTIQDPRKKSDVTSILSECSTIIDLQDGFGWLFEMVKKPTSQRVQSVEIDMESED
SVDKRKPPMVIWMNLRKTCYQIVKHSWFESFIIFVLLSGGALIFBUVHCHUQFKIQE
SVDKKKPDWVIWMNLRKTCYQIVKHSWFESFIIFVLLSGGALIFBUVHCHUQFKIQE
LLNCTDIIFHIFILEMVLKWVAFGFGKYFTSAWCCLLPIIVIVSVTTLINLMELKSF
RTLAALRELAALSQEEGMKVVVNALIGAIPALINVLINVCLIFFILVFCILGVYFFSGKF
RTLAALRELAALSQEEGMKVVVNALIGAIPALINVLINVCLIFFILVFCILGVYFFSGKF
                                                                                                    GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
IYAAVDSTEKEQQPEBESNSLGYIYFVUFIIFGSFFTLNLFIGVIIONENQQOKKLGG
QDIFWTEEQKKYYNAMKKLGSKKPQKPIPRPLNKCQGLVFDIVTSQIFDIIIISLIILI
NMISMMAESYNQPKANKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
VLLSIVSTMISTLENQEHIPFPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
PSLFNIGLLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSWLCLFQLSTSAG
WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
TEESEDPLGEDDFDIFYEVWEKFDPEATQFIKYSALSDFADALPEPLRVAKPNKYQFL
VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFWEANPLKKLYEFIVT
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IPLRTETVFFALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQ01FM
GSLAUKCISRDCKNISUBEAYDHCFEKKENSPEFKWGIWHMGNSACSIQYECHTTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mddrcypv1fpdernfrpftsdsLaA1eKr1A1QKEKKKSKDQT
GEVPQPRPQLDLKASRKLPKLYGD1PRELIGKPLEDLDPFYRNHKTFMVLNRKRT1YR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="voltage-gated sodium
/protein_id="CAD10507.1"
/db_xref="G1:22796540"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 10
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YONG JEONG
OS Homo sapiens (human)
PN WO 0190355-A/2
PD 29-NOV-2001
PF 11-JUL-2000 WO 2000JP004629
PR 23-MAY-2000 JP 00P 152085
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEO)
PC C12N15/12, C07K14/47, C07K16/18
CC
CT
FH Key Location/Qualifiers
FT CDS (200) . (4534).
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5728
Human Bodium channel SCN12A.
BD082952
BD082952.1 GI:22628562
DP 2001327294-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kanazawa,I., Goto,J. and Jeong,S.Y. Human sodium channel SCN12A and SCN8A Patent: WO 0190355-A 2 29-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5728)
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WO 0190355-A/2.
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Human sodium channel SCN12A and
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 5728)

1 (bases 1 to 5728)

1 (bases 1 to 5728)

1 (seong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.

1 (dentification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A

Blochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                5728 bp mRNA linear PRI 15-JAN-2000 Homo sapiens voltage-gated sodium channel alpha subunit, alternate splice variant SCN12A-s (SCN12A) mRNA, complete cds. RF150882
                                                                       Submitted (12-MAY-1999) Neurology, Graduate School of Medicine, Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tokyo 113-8655, Japan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                     Direct Submission
                                                                                                                                    and Kanazawa, I.
                                                                                                                                                  Jeong,S.-Y.,
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/db_xref="taxon:9606"
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                                                                                                                                                    Hashida, H.,
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Masuda, M.,

Goto, J.

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RS Kanazawa,I., Goto,J. and Tei,Y.

Human sodium channel SCN12A

AL Patent: JP 2001377294-A 2 27-NOV-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2001327294-A/2

PN JP 2001327294-A/2

PF 23-MAY-2000 JP 2000152085

PI ICHIRO KANAZAWA,JUN GOTO, YOSHIHIRO TEI

PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00

FH Key Location/Qualifiers

FT CDS (200). (4534).
                                                                                                          4062 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 4173
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Pred. No. 1.4e-20;
0; Mismatches 16
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'map="3p21.3-p23" ...5728 'gene="SCN12A"

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Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in
Patent: US 6573067-A 41 03-JUN-2003;
                                                                                                                                                                                                                                                                                                                     Sequence 41 from patent AR340678
                                                                                                                                                                                                                  Unknown
                                                                                                                                                                                                                                                                                            AR340678.1
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nilarity 90.1%;
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WLAFLAEEEDDVEFSGEDNAQRITQPEFEQQAYELHQEKKKFJEGRVQSVEIDMRSED
EPHLTIQDFRKKSDVTSILSECSTIDLQDGFGMLPEMVPKKQPERCLPKGFGCCFCC
SVDKRKPPWVIWMNLRKTCYQTVKHSWFESFIIFVILLSGALLFEDVHLENQPKIQE
LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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HFDEHGDPLQRQRALSAVSILTITMKEGEKSQBPCLPGGENLAKYLVWNCCPQWLCV
KKVLKTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAS
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
SWPTLNTLIKIIGNSVGALGNLTVVLVIVIFIFSVVGMQLFGRSFNSQKSPKLCNPTG
PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENMWECNQEANASSSLCVIVFILITVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTLRALRPLRALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
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IAECVFTGIYIFEALIKILARGFILDEFSFLRDFWNWLDSIVIGIAIVSYIPGITIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
QDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPLNKCQGLVFDIVTSQIFDIIISLIIL
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/organism="unknown"
                                                 Location/Qualifiers
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US 6573067.
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                                                                                                      dorsal root ganglia
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AF188679
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AUTHORS
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VERSION
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DEFINITION
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Homo sapiens voltage-gated sodium channel type XI alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 6237)
Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman.
Direct Submission
Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,
Submitted (21-SEP-1999) Neurology, Yale University/VAMC, 127A,
Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two tetrodotoxin-resistant sodium channels in human dorsal root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF188679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 4004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA, complete cds.
                                  /translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT
GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFWTLNRKRTIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKUSNSUNIVD
IAECVFTGIYIFEALIKILARGFILDEFSFLEDFMNMLDSIVIGIAIVSYIPGITIKL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                                                     /gene="SCN11A"
31. .5406
GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
                                                                                                                                                                                     subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      /protein_id="AAF17480.1"
/db_xref="GI:6572950"
                                                                                                                                                                                                    /product="voltage-gated sodium channel
                                                                                                                                                                                                                       /note="NaN alpha subunit; TTX-R sodium channel"
/codon_start=1
                                                                                                                                                                                                                                                               gene="SCN11A"
                                                                                                                                                                                                                                                                                                                                            gene="SCN11A"
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                            map="3p21-p24"
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                                                                                                                                                                                                                                                                                                                                                                    ssue type="dorsal root ganglia"
.6237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type="mRNA"
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Pred. No. 1.4e-20;
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                                                                                                                                                                                                      type XI alpha
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SYFTPKKRKLFGNKKRKSFFLRESGKDQPPGSDSDEDCQKKPQLLEQTKRLSQNLSLD HFDEHGDPLQRQRALSAVSILTITMKEQEKSQEPCLPCGENLASKYLVMNCCPQMLCV

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REFERENCE
AUTHORS
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BD012082
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KEYWORDS
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  YAPAN YONG J
OS P
PD PD
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155;
                                                                                                                                                                                                                                            Homo Bapiens (human)
Homo Bapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6528)
                                                                                                                                                                            Kanazawa, I., Goto, J. and Jeong, S.Y. Human sodium channel SCN12A and SCN8A Patent: WO 0190355-A 1 29 NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                               BD012082.1 GI:22092271
WO 0190355-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BD012082
Human sodium channel SCN12A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Homo sapiens (human)

WO 0190355-A/1

29-NOV-2001

11-JUL-2000 WO 2000JP004629

23-MAY-2000 JP 00P 152085
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EPHLTIQDPRKKSDVTSILSECSTIDLQDFGWILPMVFKKQFERCLPKGFGCCEPCC
SUDKRKPRVIWMILRKTCYQIVKHSWPESFII FYLLLSSGALIFEDVHLENQQRIQE
LLNCTDIIFHIFILENVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLMLFIGVIIDNFNQQKKLGG
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NMISMMAESINQPKAMKSILDHLNWVFVVIIFTLECLIKIFALRQYFFTNGWNLFDCVV
VLLSIVSTMISTLENQEHIFPEPTLFRLVRLARIGRILHUVRAARGIRTLLFALMMSL
PSLENNIGLLLFLIMFIYAILGNWFSKUNPESGIDDIFNETFRASSMLCLFQISTSAG
WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVNAMYIAVILENFNTA
TESSEDPLGEDDFDIFYEWSKEDPBATQFIKKSALSDFADALDEPLRVAKPNKYQFL
VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMBANPLKKLYEBIVT
                                                                                                                                                  SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO,
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6165. .6170
/gene="SCN11A"
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WCRKQNLPQQKEVAGGCAAQSKDIIPLVMEMKRGSETQEELGILTSVPKTLGVRHDWT
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CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMNCVLQKRSWPFLRSFRVLRVFKLAK
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Pred. No. 1.4e-20;
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VERSION
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TITLE
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Best Local :
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4062
                                                        4002 ÁTTCCACÁGÁGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
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                           261
                                                                                                                                                                                                                                                                                                                                                                             Kanazawa,I., Goto,J. and Tei,Y.
Human sodium channel SCN12A
Patent: JP 2001327294-A 1 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
                                                                                                                                                                                                                                                                FF CC PF PR OS
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Human sodium channel SCN12A.
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1 (bases 1 to 6528)
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             TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
                                                                         ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                        23-MAY-2000 JP 2000152085
ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
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27-NOV-2001
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                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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Pred. No. 1.4e-20)
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score
and is
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409
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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409
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Match
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9:
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L: geneseqn1980s:*
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Copyright (c) 1993 - 2004
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Compugen Ltd.
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Aax60242 cDNA enco
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                Ab142420
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71.2	71.2	71.2	71.2	71.2	72.4	72.8	73.6	74	74	74	74	74.2	74.4	76.4	76.4	76.4	76.4	77.2	77.2	77.2	77.2
17.4	17.4	17.4	17.4	17.4	17.7	17.8	18.0	18.1	18.1	18.1	18.1	18.1	18:2	18.7	18.7	18.7	18.7	18.9	18.9	18.9	18.9
9112	6599	6599	6599	6596	188	8553	7555	7053	7053	7008	7008	6957	366	8509	8490	6048	6048	6586	6586	6556	6007
v	9	9	9	9	9	7	N	თ	w	9	9	ø	տ	7	σ	4.	N	7	N	N	2
AAH55823	ADB78647	ADB78648	ADB78650	ADB78646	ADB78657	ABT41821	AAQ05831	AAL42751	AAA93791	ADB78639 '	ADB78645	ADB52723	AAH55819	ACC46433	ABZ35506	AAF30825	AAV09029	ABT42021	AAV58423	AAV58419	AAV58421
Aah55823	Adb78647	Adb78648	Adb78650	Adb78646	Adb78657	Abt 41821	Aaq05831	Aal42751	Aaa93791	Adb78639	Adb78645	Adb52723	Aah55819	Acc46433	Abz35506	Aaf30825	Aav09029	Abt 42021	Aav58423	Aav58419	Aav58421
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## ALIGNMENTS

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RESULT 1
                       AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                       Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss
                                                                                                                                        Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                 WPI; 1999-562112/47.
                                                                                                                                                                                           Grose
                                                                                                                                                                                                                                                                                                                       WO9947670-A1
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Human sensory neurone specific 2a nucleotide sequence fragment #13
                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ21493 standard; cDNA; 409
                                                                                                               Claim 6; Page 67; 73pp; English.
                                                                                                                                                                                                                                             18-MAR-1998;
                                                                                                                                                                                                                                                                     18-MAR-1999;
                                                                                                                                                                                                                                                                                             23-SEP-1999.
                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                           DT,
                                                                                                                                                                                         Hick CA,
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                                                                                                                                                                                                                                            98GB-00005793.
                                                                                                                                                                                                                                                                      99WO-GB000838.
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Query Match Best Local Matches 409;

Similarity

100.0%; Score 409; DB 2; 100.0%; Pred. No. 2.2e-97; tive 0; Mismatches 0;

Length 409; Other;

Indels

0

Gaps

0

Conservative

Sequence 409 BP; 117 A; 90 C; 76 G; 126 T; 0 U; 0

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RESULT 2
AXX60242
ID AAXX6
XX AC AAXX
AC AAXX
AC AAXX
DT 11-/
XX TYF
XX TYF
XX Inel
XX
                                                                                   The present sequence encodes a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                                                                                                                                                                                                                                                                        Claim 1; Fig 3A; 90pp; French.
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                                                          neuropathy, and
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                     This is the nucleotide sequence of a partial cDNA clone which codes for a comportion (see AAY80596) of human NaN, a "previously unidentified voltage cC gated sodium channel protein that is preferentially expressed in dorsal croot ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R cc sodium current. The NaN channel cDNA was obtained from human DRG tissue CDNA by PCR amplification (see also AAX87520-22). Rat, mouse and human CC NaN nucleic acids (see AAX87600-02) and polypeptides (see AAX06596-98) cc are provided. The invention also includes expression vectors and ct transformed host cells, methods for identifying tissues and cells that cxpress NaN, methods for identifying agents that modulate NaN channel cc express NaN, methods for identifying agents that modulate NaN channel cc transformed such agents to treat acute or chronic pain, paraesthesia and chyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively condifying the behaviour of these nerve cells while not affecting other corrected that the brain and spinal cord. The gene is named SCN11a
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The present sequence is that of a partial cDNA for a novel human tetrodotoxin resistant sodium channel, termed NaN (see AAB20125). The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). A full-length sequence is given in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Proferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 8A; 162pp; English.
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Pred. No. 4.6e-25;
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                                                                                                                                                                      Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; human nervous system; chromosome 3p23-21.3; excitatory cell drug development; familial hyperglycaemia; QT extending syn
                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                               Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel subunit SCN12A-s coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 200. .4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human sodium channel subunit SCN12A-s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1043 A; 807 C; 820 G; 1030 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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Pred. No. 4.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP
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The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN1 and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21

Claim 7; Page 55-70; 118pp;

Japanese.

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RESULT 6
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Matches 155; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5728 BP; 1637 A; 1241 C; 1199 G;
                           The present sequence is that of cDNA encoding a novel human tetrodotoxin resistant sodium channel, termed NaN (see AAB20121). The cDNA was isolated from a human dorsal root ganglia tissue CDNA library by PCR amplification (see also AAR30122-23). NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of
                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                           Claim 1; Fig 11A; 162pp; English.
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nilarity 90.1%;
Conservative
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Pred. No. 5.4e-25;
0; Mismatches 16
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                                                                                                                                                                                              human tetrodotoxin
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Best Local (
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                                                        Expression vector useful for stable cloning and expression of Navl.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Navl.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other:
                                                                                                                                                                                                                                                           Gonda MA,
                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2002;
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                                                     sequence that
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                                                                                                                                                                                                                                                                                                                    (TRAN-) TRANSMOLECULAR INC
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                                                                                                                                                                                                   2003-876895/81.
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                                                                                                                                                                        ADD32194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 5860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT
                                                                                                                                                                                                                                                           Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                         2002US-0365550P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; dorsal root ganglion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
31. .5406
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/product= "Na
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90.1%;
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Pred. No. 5.4e-25;
0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          v 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; gene;
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The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or

Disclosure; SEQ ID NO 3; 125pp; English

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RESULTI 8
AAL42749
ID AAL4
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AC AAL4
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DT 19-J
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C Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a [method of making a cell or cell line that produces a Na v 1.9 cell that has cell conditions that allow expression vector; and (b) culturing the cell cunder [conditions that allow expression of Na v 1.9 sodium channel protein cell produce a sodium current into the transfected cell; (3) a method of exposing the cell or cell line produced by the method to the agent; and cell that modulates sodium current in a cell by: (a) composing the cell or cell line produced by the method to the agent, where an alteration in the level of sodium current is indicative of an agent ceapable of modulating sodium current in a cell; and (4) a recombinant ceapable of modulating sodium current in a cell; and (4) a recombinant ceapable of modulating and expression vector. The expression vectors are useful cor the stable cloning and expression the have 1.9 sodium channel currents channel at the mRNA and protein levels, and for producing sodium channel currents considered sequence encodes a human Na v 1.9 sodium channel protein, which is necessary invention.
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Best Local S
Matches 155
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                                      23-MAY-2000; 2000JP-00152085
                                                                                                     11-JUL-2000; 2000WO-JP004629
                                                                                                                                                                        29-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; n nervous system; chromosome 3p23-21.3; excitatory cell; development; familial hyperglycaemia; QT extending syndrome type 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sodium channel subunit SCN12A coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endplate disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 6528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
200. .5575
                                                                                                                                                                                                                                                                                                      'product= "Human sodium channel subunit SCN12A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.9%;
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Pred. No. 5.4
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05-AUG-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A sodium channel subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                          polyA_signal
                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                NaN; sodium channel; ion transport; mouse; dorsal root paraesthesia; hyperexcitability; therapy; Scnlla gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6528 BP; 1842 A; 1446 C; 1410 G; 1830 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 29-46; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanazawa I,
                                WO9938889-A2
                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                             Mouse sodium channel NaN cDNA.
                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                           AAX87601;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX87601 standard; cDNA; 5822 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCCACAGAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTACT
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                       /*tag= b
/note= "these bases represent nucleotides missing from
/note= "these bases represent nucleotides missing from
the sequence given in Fig 7 of the specification. The
nucleotides are included to maintain the nucleotide
numbering given in the specification for this DNA
sequence"
                                                                                                                                                                                    4201. .4260
                                                                                                                                                                                                                                  Location/Qualifiers
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90.1%;
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Pred. No. 5.6e-25;
0; Mismatches 16
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                                                                                                                                                                                                                                                                                                 ganglia; pain;
ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ganglia cDNA by PCR amplification using rat NaN-based primers (see AAX87618-19). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAX06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The prevides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The gene encoding NaN has been named Scnila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from mouse trigeminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1999;
              Key
                                                                                                                 Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; pain;
                                                                                                                                                                                    30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5822 BP; 1483 A; 1411 C; 1352 G; 1515 T; 0 U; 61 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 7A1-3; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYYA ) UNIV YALE.
                                               Mus musculus.
                                                                               diagnosis; ss.
                                                                                                                                                   Mouse sodium channel NaN cDNA
                                                                                                                                                                                                                                                      AAF30103 standard;
                                                                                              paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                           3824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is the nucleotide sequence of an isolated nucleic acid which encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-479168/40
                                                                                                                                                                                                                                                                                                                                                                         321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTCTAACAGAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
                                                                                                                                                                                                                                                                                                                                                                                                           TCGTGGTTTTTATCATCTTCGGCTCATTCTTTACCCTGAACCTCTTTATCGGTGTTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTCCAGAGGGAAAGATGAGCAGCCGGCCTTTGAGGCGAATCTATACGCATACCTTTACT
                                                                                                                                                                                                                                                                                                                                                                        TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                         TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT
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                                                                                                                                                                                    (first entry)
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98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US002008
            Location/Qualifiers
                                                                                                                                                                                                                                                    CDNA; 5822 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5822;
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RESULT 11

XU ADD32195

ADD32195

standard; cDNA; 5822

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Gaps

320 3823 260 in the

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                                                                                                                                                                                                                                                                                                                                                                                                                      sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in
                                                                                                                                                                                                                                                                                                                                                               gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, diagnosis of disease, and in the recombinant production of NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of cDNA encoding a novel mouse tetrodotoxin resistant sodium channel, termed NaN (see AAB20124). The cDNA was isolated from trigeminal ganglia cDNA using primers (see AAB20120-21) based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN (see AAB20121). The gene encoding NaN, termed Scnlla, is located on mouse (see AAB20121).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD
                                                                                                                                                                                                                                                                                                         Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                               polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 7A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-103147/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUL-2000; 2000WO-US019342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001
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                                                                          3824
                                                                                                                                                    3764 ATTCCAGAGGGAAAGATGAGCAGCCGGCCTTTGAGGCGAATCTATACGCATACCTTTACT
                                      321
                                                                                                                                                                                          202
                                                                                                                                                                                                                                 126;
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB20124.
                                                                                                TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGAGCAATTCACTCGGTTACATTT-CT
                                  TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                          TCGTGGTTTTTATCATCTTCGGCTCATTCTTTACCCTGAACCTCTTTATCGGTGTTATTA
TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT
                                                                                                                                                                                                                                   Conservative
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5789. .5794
/*tag= b
5800. .5822
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                                                                                                                                                                                                                                                   21.5%;
73.3%;
                                                                                                                                                                                                                               Score 88; DB 4; Length 5822; Pred. No. 8e-13; O; Mismatches 45; Indels
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expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron; mouse; gene; ss

Mouse Na v 1.9 sodium channel protein encoding cDNA

SEQ ID

NO:5

15-JAN-2004 ADD32195;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an expression vector comprising a nucleic caid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a |method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under |conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and cell basauring sodium current following exposure to the agent; where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell in the cell of sodium current is and cell and (4) a recombinant cell in the cell of sodium current in a cell; and (4) a recombinant cell in the cell of sodium current in a cell; and (4) a recombinant cell in the cell of sodium current in a cell; and (4) a recombinant cell in the cell of sodium current in a cell; and (4) a recombinant cell in the cell of sodium current in a cell and (4) a recombinant cell in the cell of sodium current in a cell and (4) a recombinant cell in the cell of sodium current in a cell sodium current in a cell cell in the c
                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                    cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a mouse Na v 1.9 sodium channel protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                             Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 5; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                                                                                                                                              is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TRAN; ) TRANSMOLECULAR INC
                                                                                                                                                                                                                                       Local Similarity
                                                                                                    3764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2003-876895/81.
                                                   261
                                                                                                                                                        202
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                                                                                                                                                                                                              126;
                                TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                  ATTTCTAACAGAAAGAACAACCAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
TCGTGGTTTTTATCATCTTCGGCTCATTCTTTACCCTGAACCTCTTTATCGGTGTTATTA 3883
                                                                                                 ATTCCAGAGGGAAAGATGAGCAGCCGGCCTTTGAGGCGAATCTATACGCATACCTTTACT
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                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                              21.5%;
                                                                                                                                                                                                           0
                                                                                                                                                                                                                              Score 88; DB 9;
Pred. No. 8e-13;
                                                                                                                                                                                                         Mismatches
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272 ATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCATTGACAACTTC

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RESULT 12
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                                                                                                                                                                                                                                                                 Matches 137;
                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     individual's predisposition to epilepsy and/or development of epilepsy, as well as predicting the individual's response to medication. The method comprises determining the genotype of at least one gene selected from SCNIA, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all sodium channel genes located on chromosome 2. The idiopathic generalised epilepsy (IGE) gene is more specifically localised on chromosome 2q23-q31. Compounds identified as modulators of the biological activity of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy or other neurological disorders. They have anticonvulsant and neuroprotective activities. AAH55763 to AAH56164 and AAB99679 trepresent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers, oligonucleotides and proteins given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining a predisposition to epilepsy and/or development of epilepsy comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA variant, equivalent, or mutation which shows a linkage disequilibrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; epilepsy; chromosome 2; SCNIA; SCN2A; SCN3A; identification; diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective; ds.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method (M1) of determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 183; 268pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-1999;
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                                                                                                                                                                                                   153 GAATGCTTATATTTTTCTCCAGTAATTGTTTTTTTTCTCTTATTAAAAAAATTTTCTAACAG
                                                                                                                                                                                                                                                                                                   Similarity
   GTTAAACTTCAGCCTGTATATGAAGAAAATCTGTACATGTATTTATACTTTGTCATCTTT
                                                                 AAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCTTCGTAGTCTTT
                                                                                                                                     GATTTAGTGTAAGTATTTATAGTATTTTCATATTATTTAATATTTCAATATCATTTAG
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                BP; 194 A; 117 C; 102 G; 224 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                Score 85.2; DB 5;
Pred. No. 2.1e-12;
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RESULT 14
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                                                                                                                                                                                                                                        Matches 123;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a type 5 sodium channel protein designated PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60244 standard; cDNA;
                                                                                                                                                                                                                                                                                                 Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 5A-E; 90pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dietrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuropathic pain; migraine; headache; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stabilised cDNA encoding type 5 sodium channel protein designated PN5
                                                                                                                                                                                                                                                                                                                             neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                    3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
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                                                                                                                                                                                                            202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding sodium channel of the nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACCAGCAGAAAAAGAAGATAAGTAT 366
                                                                                                                      TTGTGGTTTTTATCATCTTCGGCTCCTTCTTTACCCTGAACCTCTTTATCGGTGTTATTA
                                                                                                                                                                                 ATTCCAGAGAGAAAGACGAGCCGGACTTTGAGGCGAACCTCTACGCGTATCTCTACT
                                                                                                                                                                                                           ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGA-GAGCAATTCACTCGGTTACATTTCT
                                                            TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATCTTCAT 3937
                                                                                      TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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                                                                                                                                                                                                                                        Score 83.2; DB 2
Pred. No. 1.4e-11
0; Mismatches 4
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Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic aci sequence that encodes a mammalian Nav1.9 sodium channel protein or it
                                                                                                                                                                                                                                                                                                                                                02-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                WO2003080570-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Na v 1.9 sodium channel protein encoding cDNA SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD32209 standard; cDNA; 5298
                                                                                                                                                                                                Claim 13; SEQ ID NO 19; 125pp; English
                                                                                                                                                                                                                                                                                Gonda MA,
                                                                                                                                                                                                                                                                                                               20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                                                                                                                20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD32209;
                                                                                                                                                                                                                                                                                                (TRAN-) TRANSMOLECULAR INC
                                                                                                                                                                                                                                                                2003-876895/81.
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                                                                                                                                                                                                                                                        ADD32210
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                 'product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                 .5298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         rat;
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protein or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss
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The present invention describes an expression vector comprising a nucleic control of the present invention describes an appression vector comprising a nucleic carid sequence that encodes a mammalian Na v.9 sodium channel protein or cits fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pcMv-rNaN-GFP, plG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 codium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell cunder conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of correcting the cell or cell line produced by the method to the agent; and cell exposing the cell or cell line produced by the method to the agent; and capable of modulating sodium current is indicative of an agent capable of modulating sodium current is indicative of an agent capable of modulating sodium current is a cell; and (4) a recombinant cell capable of modulating sodium current in a cell; and vectors are useful cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a rat Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.

Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other

맑 S Query Match Best Local ( Matches Similarity **ATTCCAGAGAAAAGACGAGCAGCCGGACTTTGAGGCGAACCTCTACGCGTATCTCTACT** ATTTCTAACAGAAAGAACAACCAGCCAGAGTTTGA-GAGCAATTCACTCGGTTACATTTCT Conservative 20.0%; Score 81.6; DB 9; Pred. No. 3.7e-11; 0; Mismatches 49 49; Length 5298; Indels ۲ Gaps 3802 260

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261

TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320

cells in the

brain and spinal cord. The NaN gene has been named

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Best Local Similarity 70.9%;
Matches 122; Conservative
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                                                                   3843
                                                                                                                                     3783 ATTCCAGAGAGAAGACGAGCAGCCGGACTTTGAGGCGAACCTCTACGCGTATCTCTACT
                                                                                                                                                                     202 ATTTCTBACAGAAAGAACAACAGCCAGAGTTTGA-GAGCAATTCACTCGGTTACATTTCT
                                                                   TTGTGGTTTTTATCATCTTCGGCTCCTTTTACCCTGAACCTCTTTATCGGTGTTATTA
 TTGACAACTTCAATCAGCAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 3954
                        TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                       TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                       0,
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Pred. No. 3.8e-11;
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Search completed: March 22, Job time: 297.047 secs 2004, 16:13:18

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1    /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2    /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3    /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4    /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5    /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/ Cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
   5 US-10-388-470-6
5 US-10-388-470-1
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6 US-09-840-125-3
0 US-09-840-125-3
14 US-10-077-054-1
5 US-10-333-191-3
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39.8 39.8 8888	43.2 43.2 40	460.6 460.2 60.2	6 6 6 6 0 0 0 0 6 6 6 6		68 67.4 67.4	69 68.8 68.8
9.7		14.8 14.7 11.3 10.6	14.9 14.8 14.8		16.5 16.5 16.5	16.9 16.8 16.8 16.8
3596 3632 3632 7791	3673778 6639 550	6030 6318 5482 19734	6315 5889 5922 5997	6404 6328 7028 6027	142 8530 6348 6361	3033 6452 142 473
16	10 14	9 10 14	9 9 10	15440	110	10 9 9
US-10-435-804-3 US-10-435-804-3 US-10-435-804-4 US-10-435-804-4 US-10-375-253-35	US-10-312-841 US-09-917-800A- US-09-814-353-	US-09-930-871-11 US-09-428-371-1 US-10-429-681-2 US-10-311-455-1906	US-09-428-371-2 US-09-930-871-3 US-09-930-871-13 US-09-930-871-1	09-457-571 10-161-803 10-101-510 10-297-022	US-09-864-761-30523 US-10-220-120-104 US-09-919-03-366 US-10-161-803-61 US-09-457-571-13	US-09-457-571-1 US-09-457-571-9 US-09-64-761-20706 US-09-864-761-3944 US-09-864-761-13959
Sequence 5. Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 35, Appl	⊢e	11, e 1, e 2, e 19	Sequence 2, Appli Sequence 3, Appli Sequence 13, Appl Sequence 1, Appli	60,	30523 e 104, e 366, e 61,	Sequence 1, Appli Sequence 9, Appli Sequence 20706, A Sequence 3944, Ap Sequence 13959, A

## ALIGNMENTS

a a

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RESULT 1

US-10-388-470-6

US-10-388-470-6

Sequence 6, Application US/10388470

Publication No. US20030228662A1

APPLICANT: Waxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia

FILE REFERENCE: 44574-5004-01-US

CURRENT FILING DATE: 2003-03-17

PRICH APPLICATION NUMBER: US/10/388,470

CURRENT FILING DATE: 1999-07-16

PRICH APPLICATION NUMBER: US/09/354,147C

PRICH APPLICATION: US/09/354,147C

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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
              Sequence 4, Application US/10388470
Publication No. US20030228662A1
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SEQ ID NO 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dib-Hajj,
APPLICANT: Waxman,
CURRENT APPLICATION NUMBER: US/10/388,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: full length cDNA sequence
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LOCATION: (31)..(5403)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
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Pred. No. 2.3e-25;
""amatches 16;
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US-10-388-470-1
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                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 1
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Best Local
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PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/09/354,147C PRIOR FILING DATE: 1999-07-16 PRIOR APPLICATION NUMBER: US 60/072,990 PRIOR FILING DATE: 1998-01-29
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/388,470 CURRENT FILING DATE: 2003-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn
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LOCATION: (5804)
OTHER INFORMATION: cDNA sequence of mouse NaN, n = a or c or g
NAME/KEY:
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LOCATION: (19)..(5313)
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ORGANISM: Mus musculus
FEATURE:
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                                                        LOCATION: (41)..(5)
OTHER INFORMATION:
                                                                                                                                                        TYPE: DNA
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                                                                                            NAME/KEY:
                                                                                                                    FEATURE
                                                                                                                                    ORGANISM: Rattus norvegicus
                                      FEATURE
                                                                                                                                                                        ENGTH:
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(1996)..(4042)
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DN: cDNA sequence
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Pred. No. 6.6e-13;
                                                            for rat
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US-10-388-470-1
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                                                                                                    RESULT 6
US-09-896-994-1
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; LOCATION: (1)..(6048)
US-09-840-125-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09840125
Patent No. US20020061524A1
GENERAL INFORMATION:
                                       Sequence 1, Application US/09896994
Publication No. US20030074024A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 6048
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Best Local :
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Best Local Similarity 70.9%;
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CURRENT APPLICATION NUMBER: US/09/840,125
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR FILING DATE: 2000-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
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OTHER
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ORGANISM: Homo sapiens
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APPLICANT: Ken Stokes
Jos e Morissette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3783 ATTCCAGAGAGAAAGACGAGCAGCCGGACTTTGAGGCGAACCTCTACGCGTATCTCTACT
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115; Conserv
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                                                                                                                                                                                                                     CAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                            CATCATCTTTGGGTCTTTCTTCACCCTGAACCTCTTTATTGGTGTCATCATTGACAACTT
                                                                                                                                                                                                                                                                                                                                        GTATGAAGAGCAGCCTCAGTGGGAATACAACCTCTACATGTACATCTATTTTGTCATTTT
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Pred. No. 3.
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Pred. No. 8.8e-10;
0; Mismatches 46;
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US-10-077-054-1
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                                                                                                                                                                                                                              Sequence 1, Application US/10077054
Publication No. US20030157600A1
GENERAL INFORMATION:
APPLICANT: Makielski, Jonathan C
APPLICANT: Ye, Bin
APPLICANT: Ye, Bin
                                                                                   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
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Best Local Similarity
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/077,054
CURRENT FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                          TITLE OF INVENTION: Sodium Channel Alpha Subunits FILE REFERENCE: 960296.98032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
               LENGTH: 6091
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 6048 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/514,907
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REGISTRATION NUMBER: 38,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: WOOTGPEFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,994
FILING DATE: 02-011-2001
CLASSIFICATION: <Unknown>
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024Alris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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TELEFAX: (215) 568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
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Pred. No. 8.8e-10;
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; NAME/KEY: CDS
; LOCATION: (10)..(6054)
US-10-077-054-1
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Best Local Similarity
Matches 115; Conserv
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APPLICANT: WANG, YIXIN
PRICE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 1517.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
LOCATION: (8167)
OTHER INFORMATION: a, t,
                     FEATURE: modified_base
                                                                                                                           NAME/KEY: modified base LOCATION: (7477)...(7478) OTHER INFORMATION: a, t,
                                                                                                                                                                                           NAME/KEY: modified base LOCATION: (7300)...(7301) OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                            LOCATION: (7538)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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                                                                                            NAME/KEY: modified_base
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Pred. No. 8.9e-10;
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TITLE OF INVENTION: Common Polymorphism in S
TITLE OF INVENTION: Arrhythmia
FILE REFERENCE: 2323-154-II
CURRENT APPLICATION NUMBER: US/10/333,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR FILING DATE: 2000-07-20
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RESULT 10
US-10-333-191-3
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; LOCATION: (1)...(8491)
; OTHER INFORMATION: n may be
US-10-333-191-1
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 8491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (151)..(6198)
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                                                                                4569 CAACCAACAGAAGAAAAGTTAGGGGGCCAGGACATCTTCAT
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                                                                                                                   CAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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71.0%;
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Pred. No. 1.1e-09;
0; Mismatches 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCN5A Implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8490;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drug-induced Cardiac
                                                                                                                                                                                                                                                                                                                         Gaps
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GENERAL INFORMATION:

APPLICANT:

Sequence 3, Application US/10333191 Publication No. US20030235838A1

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RESULT 11
US-10-209-776-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10209776 Publication No. US20030096360A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches | 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/219,738 PRIOR FILING DATE: 2000-07-20 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/333,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Common Polymorphism in SCN5A Implicated in Drug-induced Cardiac TITLE OF INVENTION: Arrhythmia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2323-154-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1). (8491)
OTHER INFORMATION: n may be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 8491
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (151)..(6198)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/209,776
FILING DATE: 01-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:

ADDRESSEE: Syntex Corporation, Patent Department A2-200 STREET: 3401 Hillview Avenue P.O. Box 10850 CITY: Palo Alto
STATE: CA
              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/511,828

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  ZIP: 94303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sangameswaran, Lakshmi
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Herman, Ronald C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 GAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCTTCGTAGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATCATCTTTGGGTCTTTCTTCACCCTGAACCTCTTTATTGGTGTCATCATTGACAACTT
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                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fish, Linda M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delgado,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 76.4; DB 15; Pred. No. 1.1e-09;
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TISSUE TYPE: Dorsal root ganglia;
CELL TYPE: Peripheral nerve
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-209-776-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.2%;
Best Local Similarity 66.9%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10202824
Publication No. US20030176648A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                  NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4158 ATTCCGGAGAGATCAACAGTCAGCCTAACTGGGAGAACAACTTGTACATGTACCTGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Peries, Rohan
REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                         STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                           CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Concord
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER: 28340
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Pred. No. 3.7e-08;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                              Pike, P.O. Box 15437
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US-10-202-824-7
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Best Local Similarity 66.9%;
Matches 115; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                     TELEPHONE: (302) 886-7466 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-U1-2002
CLASSIFICATION: CUNKNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-UUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 6527 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PHM.70086 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4342 ATTCCGGAGAGATCAACAGTCAGCCTAACTGGGAGAACAACTTGTACATGTACCTGTACT 4401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
                                         MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wood, John N.
                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGACAACTTCAACCAACAGAAAAAAAAGCTAGGAGGCCAGGACATCTTCAT 4513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 6524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Delaware
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ZENECA Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1800 Concord Pike, P.O. Box 15437
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204..6077
CDS
                                                                  linear
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Pred. No. 3.8e-08;
0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 6524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
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NAME/KEY: CDS
LOCATION: 204..6602
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-202-824-5
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US-10-202-824-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10202824 Publication No. US20030176648A1 GENERAL INFORMATION:
  Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        TELEPHONE: (302) 886-7466
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-U1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/669,656
FILING DATE: 24-UN-1996
ATTORIEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 17.2%; Local Similarity 66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4462
                                                                                                                                                                                                                                                                                                                                                  NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wood, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4402 TÓGTCGTTTTCATÓATTTTCGGTGGCTTCTTCACGCTGAATCTCTTTGTTGGGGTCATAA 4461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4342 ATTCCGGAGAGATCAACAGTCAGCCTAACTGGGAGAACAACTTGTACATGTACCTGTACT 4401
                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Concord
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                        LENGTH: 7052 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGACAACTTCAACCAACAGAAAAAAGCTAGGAGGCCAGGACATCTTCAT 451:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ZENECA Pharmaceuticals STREET: 1800 Concord Pike, P.O. Box 15437
                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 204..6077
Conservative
                                                                                                                                                                                                            linear
                     17.2%;
Score 70.4; DB 14;
Pred. No. 3.9e-08;
0; Mismatches 56;
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Pred. No. 3.8e-08;
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    Indels
                                        Length 7052;
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202 ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCT 260

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APPLICANT: Gene Logic, Inc.

FITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILLING DATE: 2000-07-31
PRIOR PRILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-15-12
PRIOR PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/290,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR PILING DATE: 2001-05-12
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US-09-917-800A-1604
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US-09-917-800A-1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11604
LENGTH: 6822
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
                                                                                                                                                                                                                                                                                                     Matches
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PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Rattus norvegicus
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/298,884
FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/297,457 FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/295,798 FILING DATE: 2001-06-06
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                                                                                                                                                                                                                                 225 CCAGAGTTTGAGAGCAATTCACTCGGGTTACATTTCTTCGTAGTCTTTATCATCTTTGGCT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
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o. US20020119462A1
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                                                                                                                             TCGACAACTTCAACCAACAGAAAAAAAAGCTAGGAGGCCAGGACATCTTCAT 5038
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                                            AAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                CGTTCTTCACTCTAAATCTATTCATCGGTGTCATCATAGACAACCTTCAACCAGCAGAAGA 4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson, Kory
Castle, Arthur
Elashoff, Michael
AGAAGTTTGGAGGTCAAGACATCTTTAT 4720
                                                                                                                                                                                                                                                                                             17.0%; Score 69.6; DB 9; Length 6822; ilarity 66.9%; Pred. No. 6.3e-08; Conservative 0; Mismatches 49; Indels 0
                                                                                                                                                                                                                                                                                                  49; Indels 0;
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Search completed: March 23, 2004, 05:14:58

Job time : 280.501 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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Maximum DB
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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409
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/cgn2_6/ptodata/2/pna/
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n2_6/ptodata/2/pna/US080_COMB.seq:*
n2_6/ptodata/2/pna/US081_COMB.seq:*
n2_6/ptodata/2/pna/US081_COMB.seq:*
n2_6/ptodata/2/pna/US083_COMB.seq:*
n2_6/ptodata/2/pna/US083_COMB.seq:*
n2_6/ptodata/2/pna/US084_COMB.seq:*
n2_6/ptodata/2/pna/US086_COMB.seq:*
gn2_6/ptodata/2/pna/US086_COMB.seq:*
gn2_6/ptodata/2/pna/US086_COMB.seq:*
gn2_6/ptodata/2/pna/US089_COMB.seq:*
gn2_6/ptodata/2/pna/US092A_COMB.seq:*
gn2_6/ptodata/2/pna/US092A_COMB.seq:*
gn2_6/ptodata/2/pna/US093A_COMB.seq:*
gn2_6/ptodata/2/pna/US093A_COMB.seq:*
gn2_6/ptodata/2/pna/US093A_COMB.seq:*
gn2_6/ptodata/2/pna/US093A_COMB.seq:*
gn2_6/ptodata/2/pna/US095A_COMB.seq:*
gn2_6/ptodata/2/pna/US095A_COMB.seq:*
gn2_6/ptodata/2/pna/US095A_COMB.seq:*
gn2_6/ptodata/2/pna/US095C_COMB.seq:*
gn2_6/ptodata/2/pna/US096C_COMB.seq:*
gn2_6/ptodata/2/pna/US096C_COMB.seq:*
gn2_6/ptodata/2/pna/US096C_COMB.seq:*
gn2_6/ptodata/2/pna/US096C_COMB.seq:*
gn2_6/ptodata/2/pna/US097A_COMB.seq:*
gn2_6/ptodata/2/pna/US097B_COMB.seq:*
gn2_6/ptodata/2/pna/US097B_COMB.seq:*
gn2_6/ptodata/2/pna/US098B_COMB.seq:*
gn2_6/ptodata/2/pna/US098B_COMB.seq:*
gn2_6/ptodata/2/pna/US098B_COMB.seq:*
gn2_6/ptodata/2/pna/US098B_COMB.seq:*
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45. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 47. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 47. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 47. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 48. / Gan. 2 / Pra. / USS101 COMB. seq; 49. / Gan. 2 / Pra. / USS101 COMB. seq; 49. / Gan. 2 / Pra. / USS101 COMB. seq; 51. / Gan. 2 / Pra. / USS101 COMB. seq; 51. / Gan. 2 / Pra. / USS101 COMB. seq; 51. / Gan. 2 / Pra. / USS101 COMB. seq; 52. / Gan. 2 / Pra. / USS101 COMB. seq; 52. / Gan. 2 / Pra. / USS101 COMB. seq; 53. / Gan. 2 / Pra. / USS101 COMB. seq; 54. / Gan. 2 / Pra. / USS101 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 55. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 56. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS100 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. seq; 57. / Gan. 2 / Produkta / Z / Pra. / USS101 COMB. s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PRIOR APPLICATION NUMBER: GB 9805793.8

PRIOR FILING DATE: 1998-03-18

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 409

TYPE: DNA
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No.
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APPLICANT: Tate, Simon N
APPLICANT: Tate, Simon N
APPLICANT: Hicks, Caroline A
TITLE OF INVENTION: Ion Channels
FILE REFERENCE: PG3432
CURRENT APPLICATION NUMBER: US/09/646,224A
CURRENT FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                           RESULT 1
US-09-646-224A-15
; Sequence 15, Application US/09646224A
; GENERAL INFORMATION:
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VS-09-195-851-3
PCT-US09-19342-6
PCT-US99-02008-6
VS-10-388-470-6
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0 US-10-296-130-3
PCT-US00-19342-41
PCT-US03-08611-3
PCT-US03-08611-3
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PCT-US00-19342-4
PCT-US00-1934-1
US-10-388-470-4
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US-10-388-470-3
US-10-385-550-5
US-10-485-101-345
US-10-144-771-153
US-60-485-101-345
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US-10-144-771-153
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US-10-664-423-95
US-60-233-445-440
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US-60-233-33-377-48
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US-10-296-130-1
US-60-485-101-251
US-60-466-412-152254
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Sequence (37), App
Sequence (4, Appli
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Sequence (6, Appli
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Sequence (15, A
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (115159)
OTHER INFORMATION: n = A, T, C
US-60-466-412-84151
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US-60-466-412-84151
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84151
LENGTH: 115159
TYPE: DNA
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                                                                                    AGGCTCCCAACAGGGGCTATGGCTGTTAGGAAGAGGCTATGTAGTCAATGTTGCTGCTAA 120
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Pred. No. 1.1e-75;
1; Mismatches 6;
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RESULT 4

US-60-178-309-337

IS Sequence 337, Application US/60178309

GENERAL INFORMATION:

APPLICANT: BONAZZI, VIVIEN

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPILE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000208

CURRENT APPLICATION NUMBER: US/60/178,309
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; TYPE: DNA
; ORGANISM: HUMAN
US-60-178-306-658
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US-60-178-306-658
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GENERAL IMPORMATION:
APPLICANT: Bonazzi, Vivien
ITILE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACTD MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000202
CURRENT APPLICATION NUMBER: US/60/178,306
CURRENT APPLICATION NUMBER: US/60/178,306
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 1726
SOPTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 91.4
Matches 233; Conservative
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91.4%;
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Sequence 1412, Application US/60213846

[GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000703
[CURRENT APPLICATION NUMBER: US/60/213,846
[CURRENT APPLICATION NUMBER: US/60/213,846
[CURRENT FILING DATE: 2000-06-23
[NUMBER OF SEQ ID NOS: 1617
[SOFTWARE: FastSEQ for Windows Version 4.0
[SEQ ID NO 1412
[LENGTH: 3163
[TYPE: DNA
] ORGANISM: HUMAN
[INFARC: ALATO]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CURRENT FILING DATE: 2000-01-27; NUMBER OF SEQ ID NOS: 1012; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 337; LENGTH: 651; TYPE: DNA; ORGANISM: HUMAN
US-60-178-309-337
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                                                                                                                                                                                                                       Matches 157;
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Best Local S
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Best Local Similarity
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                                                                     2700 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                             2640 ATTCCACAGAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTACT
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                                                                                           TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
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TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTGGCCAAGACATTTTTAT
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91.4%;
                                                                                                                                                                                                                     33.6%; Score 137.6; DB 7
91.3%; Pred. No. 6.9e-22;
tive 0; Mismatches 14
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Pred. No. 3.5e-39;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENCODING HUMAN TRANSPORTER PROTEINS
                                                                                                                                                                                                                                                       DB 77;
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RESULT 6 US-09-195-851-3 · Sequence 3, Application US/09195851

GENERAL INFORMATION:

APPLICANT: Dietrich, Paul APPLICANT: Fish, Linda M.

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APPLICANT: Khare, Reena

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; ORGANISM: Homo sapiens
US-09-195-851-3
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PCT-US00-19342-6
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
LENGTH: 3701
TYPE: DNA
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LENGTH: 856
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Best Local
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APPLICANT: Rabert, Douglas K.
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Sangameswaran, Lakshmi
ITITLE OF INVENTION: A Voltage-Gated Nervous Tissue Sodium Channel,
ITITLE OF INVENTION: Polynucleotides Encoding Therefor, and Methods
ITITLE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE OF INVENTION NUMBER: US/09/195,851
CURRENT APPLICATION NUMBER: US/09/195,851
CURRENT FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                               Matches
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Modulation of Sodium Channels FILE REFERENCE: 44574-5004-02-W0 CURRENT APPLICATION NUMBER: PCT/US00/19342 CURRENT FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: US 09/354,147
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yale University
                                                                                                                                                OTHER INFORMATION:
-US00-19342-6
                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (11.(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
NAME/KEY: unsure
LOCATION: (922)
                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                           FEATURE:
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                                                               al Similarity
155; Conser
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ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver. 2.1
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                                                             32.9%;
ilarity 90.1%;
Conservative
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90.1%;
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                                                             Score 134.4; DB 1;
Pred. No. 4.2e-21;
0; Mismatches 16;
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Pred. No. 2.6e-21
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Sequence 6, Application US/10388470

Sequence 6, Explication US/10388470

GENERAL INFORMATION:

APPLICANT: Dib-Hajj, Sulayman

APPLICANT: Maxman, Stephen G.

TITLE OF INVENTION: Modulation of Sodium Channels in

FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/10/388,470

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/09/354,147C

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR APPLICATION NUMBER: US 60/109,402
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APPLICANT: Yale University
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NAME/KEY: unsure
LOCATION: (922)
OTHER INFORMATION: Y = C
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NAME/KEY: CDS
LOCATION: (1)..(3699)
OTHER INFORMATION: par
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TYPE: DNA
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al Similarity 90.1%;
155; Conservation
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Pred. No. 4.2e-21;
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Dib-Hajj et al.
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Sequence 910, Application US/10219051B

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation doing business as !

APPLICANT: Hospital / Bayer AG

TITLE OF INVENTION: Nucleotide sequences involved in pain

FILE REFERENCE: LeA 35693 Foreign Countries

CURRENT APPLICATION NUMBER: US/10/219,051B

CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: US 60/312,147

PRIOR APPLICATION NUMBER: US 60/312,147

PRIOR APPLICATION NUMBER: US 60/316,382

PRIOR FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: US 60/346,382

PRIOR APPLICATION NUMBER: US 60/346,382

PRIOR APPLICATION NUMBER: US 60/333,347

PRIOR APPLICATION NUMBER: US 60/333,347

PRIOR APPLICATION NUMBER: US 60/333,347
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SEQ ID NO 910
LENGTH: 5728
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Best Local
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SEQ ID NO 6
                                         Matches
                                                           Query Match
Best Local Similarity
                                                                                                                                       ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(5728)
OTHER INFORMATION: n=a, c, g or t
PUBLICATION INFORMATION UNDER: EMBL / AF150882
DATABASE ACCESSION NUMBER: EMBL / AF150882
DATABASE EMTRY DATE: 2000-01-16
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NUMBER OF SEQ ID NOS: 44
                                                                                                                        10-219-051B-910
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LOCATION: (922)
OTHER INFORMATION: y = c
OTHER INFORMATION: Leu.
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OTHER INFORMATION: partial human NaN cDNA sequence FEATURE:
                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Local Similarity 90.1%;
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ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTT-CT
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                                         Conservative
                                                        32.9%;
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                                     Score 134.4; DB 4
Pred. No. 4.8e-21;
0; Mismatches 16
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Pred. No. 4.2e-21;
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; ISSUE: 1
; PACES: 262-270
; DATE: 2000-01-15
; DATABASE ACCESSION NUMBER: GenBank AF150882
; DATABASE ENTRY DATE: 2000-01-15
US-10-296-130-3
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Matches
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LENGTH: 5728
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APPLICANT: JEONG, Secon-Yong
APPLICANT: JEONG, Secon-Yong
TITLE OF INVENTION: Human Sodium Channel SCN12A and SCN8A
FILE REFERENCE: 2002-1512A/WMC/00653
CURRENT APPLICATION NUMBER: US/10/296,130
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: PCT/JP00/04629
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: JP2000-152085
PRIOR FILING DATE: 2000-05-23
NUMBER: OF SEQ. ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAME/KEY: modified base
LOCATION: 5632
OTHER INFORMATION: n = a, g, c or t
PUBLICATION INFORMATION:
AUTHORS: Soen-Yong Jeong et al.
TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel a Subunit
TITLE: Gene, SCN12A
TITLE: Gene, SCN12A
Rionbys. Res. Commun.
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VOLUME: 267
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LOCATION: (200)..(4534)
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TTGACAACTTCAACCAACAGCAGAAAAAGTTAGGTGGCCAAGACATTTTTAT 4173
                     TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                         TCGTAGTCTTTATCATCTTTGGCCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
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RESULT 12 PCT-US00-19342-41

Application PC/TUS0019342

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 41
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS0308611 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                               Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2003-03-20 PRIOR APPLICATION NUMBER: US 60/365,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Transmolecular, Inc.
APPLICANT: GONDA, Matthew A
APPLICANT: GREENWOOD, John D
TITLE OF INVENTION: Recombinant Expression Vectors
FILE REFERENCE: 51530-5007-WO
FILE REFERENCE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (31)..(5
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA 320
                                                                     ATTCCACAGAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTACT
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90.1%;
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Pred. No. 4.9e-21;
0; Mismatches 16
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Pred. No. 4.9e-21;
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; LOCATION: (31)..(5403)
; OTHER INFORMATION: full length cDNA sequence for human NaN US-10-388-470-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-10-388-470-41
                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-60-365-550-3
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Best Local Similarity
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PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: 09/354,147
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/072,990
                                                                                                                                                    APPLICANT: Transmolecular, Inc.
APPLICANT: GONDA, Matthew A
APPLICANT: GREENWOOD, John D
APPLICANT: DIB-HAAJ Sulayman D
APPLICANT: WAXWAN, Steven G
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Navl.9 Sodium Channe
FILE REFERENCE: 51530-5007-PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G
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ORGANISM: Homo |
FEATURE:
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                                                                                                            CURRENT APPLICATION NUMBER: US/60/365,550 CURRENT FILING DATE: 2002-03-20
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Pred. No. 4.9e-21;
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Result
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Gapop 10.0 , Gapext 1.0
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Match Length
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| (ggn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-60-545-213-7269
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RESULT 2 US-60-548-091-266

Sequence 266, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001506
CUCRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27

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CAACTTCAACCAACAGCAGAAAAAGATAAGTA 356

85967 CATTTTCATCATCTTTGGGTCTTTCTTCACCCTGAACCTCTTTATTGGTGTCATCATTGA

86026 324 85966 264 1;

265 AGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCATTGA

206 CTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCTTCGT

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; ORGANISM: Homo sapiens
US-60-548-091-268
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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
                               Sequence 267, Application US/60548091

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 4855
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 268
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Matches 116; Conservat
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CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
SOFTWARE: FastSEQ for Windows Version 4.0 SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.4e-11;
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; SEQ ID NO 5535
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-5535
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; ORGANISM: Homo
US-60-548-091-267
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Best Local :
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND
FILE REFERENCE: CLOUISO6
                                                       APPLICANT: Louis POON
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REFERENCE: 117-492 / N.86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
                                                                                                                                                                                                       APPLICANT: Kenji OKUSE APPLICANT: Mark BAKER
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Similarity 71.0%;
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Similarity 73.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACCAACAGAAGAAAAGATACGGGGCCAGGACATCTTCAT 3352
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Pred. No. 1.6e-10;
0; Mismatches 36
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Pred. No. 3.7e-11;
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PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH:: 6524

TYPE: DNA ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS
LOCATION: (204)..(6074)
OTHER INFORMATION:
US-10-487-337-1

Matches |115; Query Match Best Local Similarity

Conservative

0;

Mismatches

56;

Gaps

17.2%; 66.9%;

Score 70.4; DB 6; Pred. No. 1.7e-09;

Length 6524; Indels

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APPLICANT: Kenji OKUSE
APPLICANT: Kenji OKUSE
APPLICANT: LOUIS FOON
APPLICANT: LOUIS FOON
APPLICANT: John Nicholas WOOD
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND
FILE REFERENCE: 117-492 / N. 86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
SOPTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 5874
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RESULT 8
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Best Local Similarity 74.1%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (1)..(5874)
OTHER INFORMATION:
10-487-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo
                                                                                                                                                              4189
                                                                     4249
                                                                                                                                                                                           TTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTT 316
                                                                   ATAATTGACAACTTCAATCAACAGAAAAAAAAGTTAGGGGGCCCAGGACATCTTCAT 4304
                                                                                                         ATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                              TACTTTGTCATCTTCATCATTTTTGGAGGCTTCTTCACACTGAATCTCTTTGTTGGGGTC 4248
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Pred. No. 7.4e-09;
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US-60-548-091-5558 RESULT 10

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CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 3899
LENGTH: 600
TYPE: DNA
ORGANISM: Homo sapiens
US-60-545-213-3899
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US-60-545-213-8171
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Matches
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8171
LENGTH: 600
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
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CURRENT FILING DATE: 2004-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: AM101083
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                 456
                                                                                                                                       396 GTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 GAT 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 TGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 GTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTAT 455
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                                                                                                                                                                  250 GTTACATTTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCAT
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                                                                   TGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTT
TAT 518
                                  GAT 372
                                                                                                    TGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTT
                                                                                                                                                                                                           Conservative
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Pred. No. 3.5e
0; Mismatches
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                                                                                                                                                                                                           Score 60.6; DB 7;
Pred. No. 3.5e-07;
0; Mismatches 39;
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3.5e-07;
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                                                                                                                                                                                                            39;
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321 TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372

TCGACAACTTCAACCAACAGAAAAAAAAGCTAGGAGGCCAGGACATCTTCAT

1542 ATTCCGGAGAGATCAACAGTCAGCCTAACTGGGAGAACAACTTGTACATGTACCTGTACT 202 ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGAGCAATTCACTGGTTACAT-TTCT

4401 260

320

261 TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA

TCGTCGTTTTCATCATTTTCGGTGGCTTCTTCACGCTGAATCTCTTTGTTGGGGTCATAA 4461

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US-60-545-213-2996
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5558
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 2996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2996, Applic GENERAL INFORMATION: APPLICANT: Wyeth APPLICANT: Mounts,
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -60-545-213-2996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 67.5%;
                                                                                                                                                                                                                                                                                                                                               316
                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                           CATCATGGACAACTTTGAGTACC 120
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STROKE, METHODS OF DETECTION AND USE:
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Pred. No. 0.0008;
0; Mismatches 14; Indels
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Pred. No. 0.
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                                                                                                                            of Drug
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; TYPE: DNA; ORGANISM: Homo sapiens US-60-545-213-2997
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US-60-545-213-7268
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                                                 ; TYPE: DNA
; ORGANISM: Homo
US-60-545-213-7269
                                                                                                                                                                                                                                                                                                                          RESULT 14
US-60-545-213-7269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-7268
                                                                                                             APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7268, Appli
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Sequence 7269, Appli GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 7268
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTED: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
Query Match
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CA358980 631834 NC
AL723537 AL723537
AL245614 Tetraodon
CB720975 AMGNNUC: N
CB608527 AMGNNUC: N
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CB534807 768167 MA
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wastson.wustl.edu
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                                                                                       Gallus gallus
Edukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 1151)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
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Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                      Riggs,F., de Jong,P. and Fr
Rat BAC End Sequences from
Unpublished (1999)
Other_GSSs: CH230-257H1.TJ
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                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Euthéria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGTTAGGAAGAGGCTATGTAGTCAATGTTGCTGCTAAGAAACACCTTGGTCTTCTAGA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGACAACTTCAACCAGCAAAAAAAGAAGATAAGTATTAAAAAATGTTTCTATATTGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGACAACTTCAACCAACAGCAGAAAAAGGATAAGTATCTGGGTTGTCTTGATTTGGTAAT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATTTTGTÄGGTÄGAÄGÄTCÄÄCCTAÄGTATGÄGGACÄÄCCTGTÄCATGTÄTCTTTÄTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 518)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ceil_line="UCD001, inbred 256"
/clone_lib="TAM32"
/clone_lib="TAM32"
/note="Vector: pECBAC1; Site_1: EcoRI; Site_2:
TAM32 Female Chicken library - for library and
ordering information: http://www.hbz.tamu.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Gallus gallus"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="TAM32-14H9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 123;
                                                                                                                                                                                                                                                         Library CHORI-230
                                                                                                                                                      MD 20850, USA
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                                                                                                                                                                                                                                                         MboI segment
                                                                                                                                                                                                                                                                                        Geer,K.,
Russell,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic
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                                                                                                                                                                                                                                                                                           Chen, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AUTHORS
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CC313020/c
LOCUS
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                                                                                                                                                                                                                                                                          TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAM32-16F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends.
                                                                                                                                                      Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC313020.1 GI:30707075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey
CC313020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATCTCTGTCCTCCAAAGAAGG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAATGCACTTCATGTAAGG 417
                                                                                                      quality sequence start: 7 quality sequence stop: 775. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
     /mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="TAM32-16F3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-257H1"
                                                       /organism="Gallus gallus"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _Sp6.1 TAM32 Gallus
                                                                                         .1079
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203 TTTCTAACAGAAAGAACAGCCAGAGTTTGAGAGCCAATTCACTCGGTTACATTT-CTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 CGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCAT 321
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 1079)

Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

Gallus BaC End Reads
Unpublished (2003)

Contact: Richard K. Wilson
Email: submissions@watson.wustl.edu
Insert Length: 152000 Std Error: 0
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                  Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATAATTTCAACCAACAGAAAAAAAAAGATAAGTATCTTAGGTTTCCTTCATTGCACTGA 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mt/cHORI-230 Rat (BN/SBNHed/MCW) BAC library produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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RESULT 4
BH040362
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ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCTTCGTAGTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 AATGCTTATATTTTTCTCCAGTAATTGTTTTTTTCTCTTTATTAAAAAAATTTCTAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135;
                                                                                                                                                                   Unpublished (1999)
Other_GSSs: RPCI 24-388E6.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH040362 533
RPCI-24-388E6.TJ RPCI-24 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH040362.1 GI:14819276
GSS.
                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCAACAGCAGAAAAAGATAAGTAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAGGAGCAGCCTGAATGGGAATGTAATTTATACATGTACCTGTACTTTGTGATTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (house mouse)
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/clone lib="TAM32"
/clone lib="TAM32"
/note="Vector: pECBAC1; Site_1: EcoRI; Site_2:
TAM32 Female Chicken library - for library and
ordering information: http://www.hbz.tamu.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
                                                     /db_xref="taxon:10090"
/clone="RPCI-24-388E6"
                                                                                                                                                          Location/Qualifiers
                                     /sex="Male"
                                                                                    (mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%;
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Pred. No. 2.7e-07;
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RPCI-24-388E6,
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 TTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112;
                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
trimmed with the aid of the trim_alt
cross_match_v0.990329.
Plate: FQY8073 row: B column: 10
Seq_primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A second set of bovine ESTs from Unpublished (2003) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, T.P.L., Roberts, A.J., Wray, J.E. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB457889 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
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AGATTCCCGAAAGCCTGATGAGCAGCCTAAGTATGAGGACAACATCTACATGTACATCTA
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                                                                                                                                         /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."
                                                                                                                                                                                               /lab_host="DH10B"
/clone_lib="MARC
/note="Vector: pc
                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                organism="Bos taurus"
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                                                                                                                                                                                                                                            tissue_type="pooled"
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                                                                               19.4%;
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Pred. No. 1.6e
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L.6e-06;
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Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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Gallus gallus (chicken)
Gallus gallus
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603858576F1 CSEQCHN75 Gallus
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Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biomolecular Sciences
University of Manchester Institute of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PO Box 88, Manchester, M60 1QD,
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 AGCAATTCACTCGGTTACATTTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTC
                                     ATGGATATTATGTATGCTGCAGTTGATTCAAGAGATGTAGAAGATCAACCTAAGTATGAG
                                                                      (bases 1 to 692)
                                                                                                            Conservative
                                                                                                                                                                                          /note=Torgan: trunks; Vector: pBluescript II KS(+);
/note=Torgan: trunks; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: Notl; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="ChEST866g20"
/dev_stage="36"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="CSEQCHN75"
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                                                                                                                           19.4%;
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Pred. No. 1.5e-06;
0; Mismatches 73
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277 GACAACCTGTACATGTATCTTTATTTGTCATCTTTATCATATTTGGATCATTCTTTACAT 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: gwaldbieser@ars.usda.gov
Single pass sequencing. Bases called with Phred v0.000925.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 Experiment Station Road, Stoneville, Tel: 662 686 3593
Fax: 662 686 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catfish Genetics Research Unit USDA-Agricultural Research Service
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
Contact: Waldbieser GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nonneman, D.J. and Waldbieser, G.C.
Characterization of a brain cDNA library from adult channel catfish (Ictalurus punctatus)
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Ictalurus punctatus cDNA clone IpCGBr1_10_C01_21_06Mar00_006 5',
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [ctaluridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctalurus punctatus (channel catfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCAGGATATATTTAT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                          TCGTCATCTTCATCTTCGGCTCATTCTTCACACTGAATCTGTTTATTGGTGTCATCA
                                                                                                                                                                                       ATTCCAGAGAGGTTGAAGATCAACCGAAGTATGAAGATAATCTCTACATGTACATCTATT
                                                                                                                                                                                                                                          ATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TTCT
TCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGATATCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 480
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="Ictalurus punctatus Brain1 primary library"
/note="Organ: brain; Vector: pSport1; Site_1: Sal 1;
Site_2: Not 1; Primary library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IpCGBr1_10_C01_21_06Mar00_006"
/sex="female and male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="USDA103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:7998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Ictalurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ictalurus.
                                                                                                                                                                                                                                                                                                              19.2%;
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                              Score 78.4; DB 12; Pred. No. 2.4e-06;
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                                                                                                                                                                                                                                                                                                                                    Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                            Gaps
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AK083220
LOCUS
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Best Local S
Matches |119
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                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         155
                                                           Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: 6630029C19 product: sodium channel, voltage-gated, type VIII, alpha polypeptide, full insert sequence. AK083220 GI:26101130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue.Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13998 row: c column: 04
High quality sequence stop: 596.
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AGENCOURT 8926526 NIH MGC 94
5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
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EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 CTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCATTGGCGTTAT
                                                                                                                                                                                                                                                                                                                              CATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
                                                                                                                                                                                                                                                                                                                                                                         CTTCGTCATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATTCCCGAAAGCCGGACGAGCAGCCTGATTATGAGGGCAACATCTACATGTACATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TT
                                                                                                                                                                                                                                                                                        CATCGACAATTTCAATCAACAGAAGAAAAAGTTTGGAGGTCAGGACATCTTCAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence
                                      musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus (house mouse)
                                                         CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 Mb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lb="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:6469275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.6;
Pred. No. 7.
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1es 54;
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    Euteleostomi;
                                                                                                                                                                                     HTC 20-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                         274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

E 6 (bases 1 to 4675)

RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Koya, S., Kurihara, C., Matcuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakati, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y.

Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Haradda, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
                                                                                                                                                                                                         Please visit our web site for further
                                                                                                                                                                                                                                                                              Division of Experimental Animal Research
                                                                                                                                                                                                                                                                                                              Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                             prepare mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                   library was prepared and sequenced in Mouse Genome
organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                         genome.gsc.riken.go.
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ciyama, J., Nishi, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagaoka, S., Sasaki, N., Carninci, P.,
                                                                                                                                                                                                                                                                                  in Riken
                                                                                                                                                                                                                                                                                                                                                  Research Group
                                                                                                                                                                                                                                                                                     contributed to
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus SCN0A gene, v
genomic survey sequence.
AV416501
AV416501.1 GI:39772461
GSS.
                                                                                                                                                                                                                                                                                                        Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                   based on alignment
                                                                                                                                                                                                                   sequence was made by sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sodium channel, voltage-gated, type VIII, ;
polypeptide (MGD|MGI:103169, GB|NM_011323,
BLASTN, 99%, match=3589)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:C630029C19"
/db_xref="MGI:2417601"
/db_xref="taxxon:10090"
/clone="C630029C19"
                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                       Location/Qualifiers
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<1. .3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse
                  'locus_tag="HCM5911"
                                         gene="SCN8A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.5%;
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, VIRTUAL
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                                                                                                                                                                                   200 AAATTTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACAT-TT 258
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted, MD 20850, USA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                AGATTCCCGGAAGCCTGATGAGCAGCCTAAGTATGAGGACAATATCTACATGTACATCTA 4328
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CATTGATAACTTCAATCAACAAAAGAAAAAGTTCGGAGGTCAGGACATCTTCAT 4442
                         CATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTTGAT 372
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                                                                        CTTTGTCATCTTCATCATCTTCGGCTCCTTCTTCACCCTGAACCTGTTCATTGGTGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence was made by sequencing based on alignment
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                               organism="Pan troglodytes"
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Pred. No. 4.9e-06;
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Pred. No. 4.9e-06;
0; Mismatches 54;
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13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-HN0031-
221100-012-f02&t3=2000-11-22&t4=1)
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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RC1-HN0031-221100-012-f02
BQ359333
BQ359333.1 GI:21026997
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                         GTTACATTTCTTCGTAGTCTTTATCATCTTTGGCTCATTCTTCACTCTGAATCTCTTCAT
                                                                                                                                                                                       TGGCGTTATCATTGACAACTTCAACCAACAGCAGAAAAAGATAAGTATCTGGGTTGTCTT
                                                                                                                                                                                                                                 GTACCTCTACTTTGTCATCTTCATCATCTTTGGCTCCTTCTTCACCCTCAACCTCTTCAT
                                                           TAT 388
                                                                                                     GAT 372
                                                                                                                                               TGGCGTCATCATTGACAACTTCAACCAGCAGAAGAAGAAGTTAGGGGGGAAAGACATCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Organ: head_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                         tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/dev_stage="Adult"
/clone_lib="HN0031"
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'mol_type="mRNA"
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75.6%;
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Pred. No. 1.2e-05;
n. Mismatches 30;
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HN0031 Homo sapiens cDNA,
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RESULT 14
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                                                                                                                                                                                                                                                                   324 ACAACTTCAACCAACAGCAGAAAAAGATAAGTATCT 359
                                                                                                                                                                                                                                                                                                                                                                        283 TTCTTTAGGTAGAATTACAACCCAAGTATGAAGACAACCTGTACATGTATCTTTATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                          204 TTCTAACAGAAAGAACAACAGCCAGAGTTTGAGAGCAATTCACTCGGTTACATTTCTTCG
                                                                                                Homo sapiens SCN8A gene, genomic survey sequence. AY416499
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clones are available fr
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 366)
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CIT-HSP-2320K3.TF CIT-HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13-21
Class: BAC ends.
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Tel: 301 838 0200
Fax: 301 838 0208
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Other_GSSs: CIT-HSP-2320K3.TR
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                                                                                     AY416499.1
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Golden, K., Berry, K., Granger, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2320K3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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                                                                                     GI:39772459
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Pred. No. 1.8e-05;
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                                                                                                                                 DNA linear GSS 17-DEC TRANSCRIPT, partial sequence,
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Suh, E., Wible, C.,
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C., Shizuya,H.,
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
              Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified k
cross_match v0.990329.
                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 763)
Rexroad, C.E. and Keele, J.W.
Sequence analysis of a rainbow trout normalized cDNA library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA358980 763 bp mRNA linear EST 05-NOV-2002 631834 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT5D21_B_B11 5',
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Library made from pooled tissue from brain, gill,
spleen, muscle, and kidney."
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## REFERENCE AUTHORS TITLE Result No. SOURCE ORGANISM RESULT 1 AX017232 LOCUS DEFINITION ACCESSION KEYWORDS VERSION ဂ Ω a a JOURNAL 113.8 112.8 Score AX017232 Sequence AX017232 Tate, S.N., Grose, D.T. and Hick, C.A. Mammalian sodium channel proteins Patent: WO 9947670-A 16 23-SEP-1999; Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AX017232.1 Query Match 9 72. 8 27. 9 119911991199 . œ . 16 59975 59975 59975 59975 59975 59975 59975 59975 59975 59975 5921 103065 8530 227788 232042 247254 5874 5874 5874 5874 215113 192202 193311 5728 5728 5728 5728 167476 Length GI:10042152 6528 6528 5908 5419 from Patent ВB 10 10 10 5 AC124662 AR340647 BD217792 E36125 RNO237852 AC116038 HSA417790 AR340678 AR340646 BD217791 AX017217 BD012082 BD082951 AF109737 AC117294 AC127824 AX017232 BD138454 AR253325 AX252393 AX552195 AC095653 E36122 BD138440 Ħ AX710162 BD217793 AR340648 AC127215 AF188679 AF150882 AF118044 AF059030 585 bp WO9947670. ALIGNMENTS DNA linear BD012063 Human sod BD082952 Human sod APT50882 Homo sapi AC116038 Homo sapi AC116038 Homo sapi AR340678 Sequence AF188679 Homo sapi BD012082 Human sod BD082951 Human sod AF109737 Homo sapi AC117294 Rattus no AC1277824 Rattus no AC1277824 Rattus no AR340648 Sequence BD217793 Regulatio AF118044 Mus muscu AR340647 Regulatio AF118044 Mus muscu B36125 Nucleic aci AJ237852 Rattus no AR340646 Sequence BD217791 Regulatio AR340646 Sequence BD217791 Regulatio AR340647 Mus muscu B36127 Nucleic aci AJ237852 Rattus no AR340646 Sequence BD217791 Regulatio AR340646 Sequence BD217791 Regulatio AR340646 Sequence BD317791 Regulatio AR340640 Mammalian AF059030 Rattus no E36122 Nucleic aci AR253325 Sequence AX752393 Sequence AX710162 Sequence AF117907 Homo sapi AC104834 Mus Muscu AC134315 Lemur Cat AC134403 Mus muscu AF050735 Homo sapi AR181339 Sequence AB031389 Mus muscu AC137625 Homo sapi AX552195 Sequence AC095653 Rattus no AC128144 Rattus no AC118844 Rattus no AX017232 Sequence BD138454 Mammalian Description L39018 PAT 07-SEP-2000 Rattus norv

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1 (bases 1 to 585)

Grose, D. T., Hick, C.A. and Tate, S.N.
Mammalian sodium channel protein
Patent: JP 2002508941-A 15 26-MAR-2002;
GLAXO GROUP LTD
OS Homo sapiens (human)
PM JP 2002508941-A/15
PD 26-MAR-2002
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PI DAVID THOMAS GROSE,CAROLINE ANNE HICK,SIMON NICHOLAS TATE E
C12N15/09,A61K45/00,A61P17/04,A61P25/02,C07K14/705,C07K16/28, PC
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1. .585
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 3.9e-131;
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RESULT 4
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Best Local Similarity
Matches 480; Conserv
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OS Homo sapiens (human)
WO 0190355-A/2
PD 29-NOV-2001
PT 11-JUL-2000 WO 2000JP004629
PR 23-MAY-2000 JP 00P 152085
PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
PC C12N15/12, CO7K14/47, CO7K16/18
CC LOCALION/Qualifiers
FT CDS (200). (4534).
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1 (bases 1 to 5728)

Kanazawa, I., Goto, J. and Jeong, S.Y.

Human sodium channel SCN12A and SCN8A.

Patent: WO 0190355-A 2 29-NOV-2001;
BD082952
Human Bodium channel SCN12A.
BD082952
BD082952.1 GI:22628562
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.1e-92;
0; Mismatches 27;
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Human sodium channel SCN12A
Patent: JP 2001327294-A 2 27-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
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1 (bases 1 to 5728)
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27-NOV-2001
23-MAY-2000 JP 2000152085
ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
CC12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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93.2%;
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Pred. No. 1.1e-92;
0; Mismatches 27;
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Tokyo University, 7-3-1 Hongo, Bukyo-ku, Tokyo 113-8655, Japan
Location/Qualifiers
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1 (bases 1 to 5728)

Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I.

Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCNI2A

Biochem, Biophys. Res. Commun. 267 (1), 262-270 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jeong, S.-Y.,
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         CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
                                                     TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT
                                                                                                 TACCTAAACCATGATTGGCTTGATGGCCTAAATATACAACCCAACCCCAAAGCCATGGAAT 129
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                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDYNYTNYDDNIGWSFLAMFRLMTODSWEKLYQOTLRTTGLYSUFFFITVIFLGSFYLI
NITLAVVTMAYEBQNKOVAAB IBAKEKNFQBAQQLIKEBKEALVAMGIDRSSLTSLET
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TVSCLRHWHMGDFWHSFLVVFRILCGEWIENNWECMGEANSSSLCVVVFILTIVIG
TVSCLRHWHMGDFWHSFLVVFRILCGEWIENNWECMGEANSSSLCVVFFILTIVIG
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MCRKKONLFOALCHSGCAAQSKDIIPLMMEMKRGSTQEELGIITSVEKTLGVRHDWT
                                                                                                                                                                                                                                                                                                                                                                                                            WLAPIABEEDDVEFSGEDNAQRITQPEPEQQAYELHQENKKFTSQRVQSVEIDMFSED
EPHLTIQDPRKKSDVTSILSEGSTIDLQDGFGWLDEMVPKKQPEGCLEKGGFGCG
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LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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/product="voltage-gated sodium channel alpha subunit,
alternate splice variant SCN12A-s"
/protein_id="AAR74980.1"
/db_xref="GI:6693705"
/translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT
                                                                                                                                                                                                                                                                                                                                        RTLRALRPLRALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVPOPRPOLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKTIIR
FSAKHALFIGOPNSIRSLAIRVSVHSLFSMFIGTVIINCVPKATGPAKNSNSNNTD
IAECVPTGIYI FEBALIKILARGFILDEFSFLANDPMNHLDSIVIGIAIVSYIPGITIK
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                                                            QDIFMTEEQKKYYNAMKKLGSKKPQKFIFRFLNKCQGLVFDIVTSQIFDIIISLIII
NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
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gene="SCN12A"
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chromosome="3"
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mol_type="mRNA"
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                                                                                                                                                Score 425.8; DB 9
Pred. No. 1.1e-92;
0; Mismatches 27
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JOURNAL
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                                                                                          Submitted (07-OCT-2003) Genome Center, University of Washi
Box 352145, Seattle, WA 98195, USA
On Oct 7, 2003 this sequence version replaced gi:21622736.
                                                                                                                                                                                                                Submitted (28-JUN-2002) Genome Center, Univ. Box 352145, Seattle, WA 98195, USA 4 (Dases 1 to 167476) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Buckley, D., Kibukawa, M.,
                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (23-MAR-2002) Genome Center, University
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 167476)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
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Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                   and Haugen, E.D.
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Kaul,R.K., Olson,M.V., Raymond,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Mammalia; Eutheria;
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                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAAGTTGCTAGGAGATA-----GAGAGTAATTTCTGTTCCCTTAACTCACTACACAA 4738
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                               Center: University of Washington Genome Center Center Code: UWGC
                                                                                ----- Genome Center
         site: http://www.genome.washington.edu
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Primates;
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me 3 clone
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Catarrhini;
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                                                                                                                                                  University of Washington,
                                                                                                                                                                                                                                                                                                                       University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi; i; Hominidae; Homo.
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linear

PRI 07-OCT-2003

4684

4624

4564

Rouse, G., Wu, Z., Raymond, C. and

Rouse, G., Kibukawa, N

Wu,

, Z., Raymond, C.

Rouse, G., Wu, Z. Raymond, C. and

of Washington

4771 4809 4878 4771 184 <800	SeqDerMap         FngrPrnt         SeqDerMap         FngrPrnt         SeqDerMap           8696         8629         2732         2741         2234           6         <800         6382         6514         2067           2248         2299         512         <800         5097           9345         9792         449         <800         2317           2016         2003         2707         2741         2813	Validation:  uence has been validated by Multinting. Comparison of the experint sequence predicted fragmes with sequence predicted fragmetronically-digested sequence contin order to accurately represent agments below a variable cutoff resolved in the fingerprint and able. There are no significant x the experimental and predicted value are separated by dashed lines.  ORI	annotated with sequence by the Phrap assembly pro 40 are expected to have 9. Base-by-base quality le from the GenBank flat s part of this entry's Assished as follows unless her double-stranded or secretary was made to resolvent was made to resolvent plasmid subclone or neglasmid subclone or neglasmid subclone or neglasmid subclone or nembly was confirmed by 1	Contact: uwgchtgs@u.washington.edu
2550 2008 2550 2550 2550	FngrPrnt 2259 2008 5007 2744	gest  t and t And r BAC.  800 bp)  ies ered	ž.	erlap
324 1141 1141 1146 3446 3569 3569 11229 7414	7213	5 <800 438 3 2686 11436 9 2686 5528 9 2686 475 9 8629 2310 9 8629 2317 1 <800 391	9211 5478 <800 240 2299 5050 2003 1053 <800 3231 1370 86 <800 5444 1560 1265	6560 4721 4771 727 3447 179 <800 7123 3091 2078 <800 1891 <800 1891 <800 8072 5088 3674
<pre>&lt;800</pre>	2486 2486 14 4240 879 879 317	<pre>&lt;800</pre>	5397 5748 6106 <800 953 943 4878 4629 1068 178 <800 3264 1222 1220 <800 694 <800 5397 3022 3007 1228 4079 3992	4667 2738 2744 4667 4704 4629 <a href="#">2738</a> 2744 4629 <a href="#">2749</a> 2649 2744 7158 2550 2550 7158 2550 2550 2040 5020 4862 1888 6949 6960 8171 4636 4629 <a href="#">8800</a> 3539 604 <800

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REFERENCE
AUTHORS
                                                                                                                                                                                                      HSA417790
LOCUS
                                                                                                            SOURCE
ORGANISM
                                                                                                                                         ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                          RESULT 7
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                                                                                                                                                                       5419 bp mRNA linear Homo sapiens mRNA for voltage-gated sodium channel AJ417790
                                                                                                                                       AJ417790.1 GI:22796539
NAVI.9 gene; voltage-gated sodium channel
                                               Blum, R., Kafitz, K.W. and Konnerth, A.
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Homo sapiens
                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                     CTGAAATAGAGTTCAATAATCATGCAGCTAATGTATTCAATGGAAATAGACAAAATTAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAGTTGCTAGGAGATAGGAGGCGGTAAATTTCTGGTTCCCCTTAACTCACTACACAA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGACTTTAAGAACCA 84341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGGACTTTAAGAACCA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATCTTTGCTTTGAGGCAATACTACTTCACCAATGGCTGGAATTTTATTTGACTGTGTG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCCTTGACCATCT - CAACTGGGTCTTTGTGGTCATCTTTACGTTTAGAATGTCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                 GGGAAGTTGCTAGGAGATA-----GAGAGTAATTTCTGTTCCCTTAACTCACTACACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT
                                                                                                                                                                                                                                                                                      ATGACTCAGAAGTTTTTGTGGTGGTAACCTGATTT 84072
                                                                                                                                                                                                                                                                                                                   ATGACTCAGAAGTTTTTGTGGTGGTAGAAAATTT 584
                                                                                                                                                                                                                                                                                                                                                   CTGAAATAGAGTTCAATAATCATGCAGCTAATGTATTCAATGGAAAATAGACAAAATTAAA 84107
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Pred. No. 7.4e-93;
D; Mismatches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blum,R.
Direct Submission
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RUTLAVUTMAYEEQNKONVARSI EAKERGHÇGEAQQLLKEEKEALWAGIDRSSLTSLET
SYFTPKKRKLFGNKKRKSFFLRESGKDQPFGSDSDBDCQKKPQLLEQTKRLSQNLSLD
HPDEHGDPLQRQRALSAVSILTITMKKDQEKSQEPCLPCGENLASKYLVMCCCPQMLCV
KKVLRTVMTGPFTELAITICII INTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
CLKIIALDPHYFRRGMNIFDSIVALLSFADVMNCYLQKRSWPFLRSFRVLFVFKLAK
SWFTLNTLIKIIGNSVGALGSLTVVLVIVIFIFSVVCMQLFGRSFNSQKSFKLCNFTG
PTVSCLRHWHMGDFWISFILVFRILCGEMIENMWECWQEANASSSLCVIVFILITVIG
KLVVLNLFIALLLNSFSNEERNGNLEGEARKTKVQLALDFFRAAFCFVGHTLEHFCHK
WCRKQNLPQOKEVAGCCAAQSKDIFELWMEMKRGSSFQEELGILTSVPKTLGVRHDWT
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/db_xref="goa:Q8NDX3"
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/tans1ation="modfcypv1federnfreffsdslaaiekriaiokekkkskdQT
/trans1ation="modfcypv1federnfreffsdslaaiekriaiokekkkskdQT
GEVPQPRPQLDLKASRKLPKLYGD1PRELIGKPLEDLDPFYRNHKTFMVLNRKRT1YR
FSAKHALF1FGDFNSIRSLAIRVSVHSLFSNF1IGTV1KCVFMATGBAKNSNSNNTD
IAECVETGIY_IFEBALIK_LIARGF1LDEFSFLADFMNMLDSIV_IGIAIVSY1PGITIKL
LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
                                                                                                                                                                                                                                                                                                        RTLRALRPLRALSQFEGMKVVVNALIGAI FAILNULLVCLIFULVFCIIGVVFFSGKE
GKCINGTDSVLNYTIITNKSQCESGRFSWINGKVNFDNVGNAYLALLQVATFKGMMDI
IYAAVDSTEKEQOPBEFSUSLGYIKFVVFIIGSFTLNLFIGVIIDNFNQQOKKLGG
ODIFMTEEQKKYYNAMKKLGSKKFQKFIFRFLNKCQGLVFDIVTSQIFDIIISLIII
NMISMAESYNQFKANKSILDHLNWVFVVIFTLESLIKIFALARGRIFTLLFALMMSL
VLLSIVSTMISTLENQERIIFFFFIFIVRLARIGRIFTLVURAARGIRTLLFALMMSL
PSLFNIGLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSMLCLFQISTSAG
                                                                                                                                                                                            WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
TEESEDPLGEDDFDIFYEVWEKFDPEATQFIKYSALSDFADALPEPLRVAKPNKYQFL
VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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EPHLTIQDRRKKSDVTSILSECSTIDLQDGFGWLPEWVPKKQPERCLERGFGCCFPCC
SVDKRKEPBVIMWNLKKTCYQIVKHSWFESFITVILLSSGALIFEDVHLENQPKIQE
LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
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/protein_id="CAD10507.1"
/db_xref="GI:22796540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     excitation"
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/cell_line="SH-SY5Y"
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.5419
Length
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Matches 4128 TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT 4186 130 CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189 192; Similarity Conservative 27.9**%**; 93.7**%**; Score 163.4; DB 9; Pred. No. 3.7e-29; 0; Mismatches 11; Indels 2; Gaps 2

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Sequence 41
AR340678
AR340678.1
                                                                                                                                                                                            6237
Homo sapiens voltage-gated sc (SCN11A) mRNA, complete cds.
AF188679
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Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal
Patent: US 6573067-A 41 03-JUN-2003;
Location/Qualifiers
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 6237) Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A., Wood,P.M. and Waxman,S.G.
                                                                                                                                                                                 AF188679
AF188679.1 GI:6572949
                            20047838
                                    ganglion neurons
FEBS Lett. 462 (1-2),
                                                               Two tetrodotoxin-resistant sodium channels in human dorsal root
                                                                                                                                           Homo sapiens
                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified
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                                                                                                                                                                                                                                                                                                                   GTCGTGCTTCTTTCCATTGTTAGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
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(bases 1 to 6237)
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41 from patent US 6573067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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93.7%;
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Pred. No. 3.6e-29;
                                        117-120
                                                                                                                                                                                                                       sodium
                                                                                                                                                                                                                                   gd
                                                                                                                                                                                                                      channel type
                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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ype XI alpha subunit
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TITLE
Best Local Sir
Matches 192;
                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \label{eq:discrete_discrete_discrete} \begin{array}{lll} \text{Dib-Hajj,S.D., Tyrrell,L., Cummins,T.R., Black,J.A. and Waxman,S.} \\ \text{Direct Submission} \end{array}
                                      Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLNLKCI SROCKNI SNPEAYDHCFEKKENSPEFKNCGI WMGNSAGSIQYECKHTKIN
PDYNYTNEDBYGWSPLAMPRLMTQDSWEKLYQQTLRTTGLYSVEFFI LVUI FLGSEYLI
NLTLAVVTMAY EEQNKNVAAE I EAKEKMPQBAQQLLKEEKEAL VAMGLDR SSLTSLET
SYFT PKKRKLFGNKKRKSFFLKESGKKOPPGSDSDEDCQKKPQLLEQTKRLSQNLSLD
SYFT PKKRKLFGNKKRKSFFLKESGKKOPPGSDSDEDCQKKPQLLEQTKRLSQNLSLD
HFDEHGDPLQRQRALSAVS ILTITMKEQEKSQBFCLPCGENLASKYLVWNCCPQMLCV
KKVLRTVMTDPFTELAITIC ILITVFLAMBEHHKMEASFEKMLASKYLVWNCCPQMLCV
KKVLRTVMTDPFTELAITIC ILITVFLAMBEHHKMEASFEKMLNIGNLVFTSIFIAEM
CLKITALDPHYFRRGNIFDSIVALLSFADVNNCVLQKRSWFFLRSFRVLRVFKLAK
SWPTLNTLIKI IGNSVGALGSLTVVLVIVIT FIFSVVGMQLFGRSENSQKSPKLCWPTG
PTVSCLRHWHMGDPWHSFLVVFRILCGEMIENMECMQEANASSSLCVIVFILITVIG
KLVULNIFIALLLENSFSNEEERNGNLEGEARKTTVVQLALDFRRAFGCFWHTLEHFCHK
WCRKQNLPQQKEVAGGCAAQSKDI I PLVMEMKRGSETQEELGILTSVPKTLGVRHDWT
WLAPILABEEDDVEFSGEDNAQRI TQPBFDEQQAYELHQENKQPEGCYPCHSTLENGFCCPPC
SVDKRKPDWV WWNLEKTCYQIVCHSWFESFII FVILLSGALI FEDVHLENQPKIQE
SVDKRKPDWV WWNLEKTCYQIVCHSWFESFII FVILLSGALI FEDVHLENQPKIQE
LLNCTDI I FTHI FI LEMVLKWVAFGFGKYFTSAWCCLDFI UVIVSVTTLINLMELKSF
LLNCTDI I FTHI FI LEMVLKWVAFGFGKYFTSAWCCLDFI UVIVSVTTLINLMELKSF
LLNCTDI I FFIN FI LEGGGMYTNANI 1 GOI BDAIL NULL UVIL FEN VEGGKF
                                                                                                                                                                                                                                                                                                                                 /gene="SCN11A"
5689. .5961
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WDSLLSPMLBSKESCNSSSENCHLPGIATSYEVSYIIISFLIVVNNYIAVILKENFNTA
TESSEDPIGEDDFDIFYEVWEKFDPEBATQFIKYSALSDFADALPEPLEKKPNKYA
VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
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NMISMMAESYNQPKAMKSILDHLNMVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
VLLSIVSTMISTLENQEHIPFPPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
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GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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/gene="SCN11A"
/note="polyA_signal"
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/codon_start=1
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/mol type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                                                                                                                                                              /rpt_family="Alu-Sc'
/rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                              KGKVHCD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MDDRCYPVIFPDERNFRPFTSDSLAAIEKRIAIQKEKKKSKDQT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAF17480.1"
/db_xref="GI:6572950"
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1. .6237
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27.9%; Score 163.4; DB 9 93.7%; Pred. No. 3.6e-29; ive 0; Mismatches 11
                                                                   9
       Indels
                                                                   Length 6237;
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       Gaps
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RESULT 11
BD082951
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ORGANISM
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VERSION
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TITLE
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Human sodium channel SCN12A.
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1 (Dases 1 to 6528)

1 (Gates 1, Goto, J. and Jeong, S. Y.

Human sodium channel SCN12A and SCN8A

Patent: WO 0190355-A 1 29-NOY-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP, ICHIRO KANAZAWA, JUN GOTO, EON
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Human sodium channel SCN12A and SCN8A.
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                                                                                                                                CCATCCTTGACCATCT - CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
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                                                                                                                   GTCGTGCTTCTTTCCATTGTTAGTA 4529
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WO 0190355-A/1
29-NOV-2001
21-UTL-2000 WO 2000JP004629
11-UTL-2000 JP 00P 152085
ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG C12N15/12, C07K14/47, C07K16/18
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 3.6e-29;
0; Mismatches 11;
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AUTHORS
TITLE
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MEDLINE
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AUTHORS
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SOURCE
ORGANISM
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VERSION
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Best Local
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 Direct Submission
                    2 (bases 1 to 6528)
Jeong, S.Y., Suzuki, T.,
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                    AF109737.1 GI:6693696
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            Kanazawa, I.
                                                          20090626
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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2 (bases 1 to 6528)

1 (bases 1 to 6528)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6528 bp mRNA linear PRI 15-JAN-2000
Homo sapiens voltage-gated sodium channel alpha subunit SCN12A
(SCN12A) mRNA, complete cds.
                                                                                                                                                                                 1 (bases 1 to 6528)
Jeong,S.Y., Goto,J., Hashida,H., Suzuki,T., Ogata,K., Masuda,N.,
Jeong,S.Y., Goto,J., Uchiyama,Y. and Kanazawa,I.
Identification of a novel human voltage-gated sodium channel alpha
subunit gene, SCN12A
Biochem Biophys. Res. Commun. 267 (1), 262-270 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 3.6e-29;
0; Mismatches 11;
Hashida,H.,
Masuda, N., Goto, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 TACCTAAACCATGATTGGCTTGATGGCCTAAATATACAACCCAACCCCAAAGCCATGGAAT 129
                                               GTCGTGCTTCCTTTCCATTGTTAGTA 274
                                                                                                                                                                                                                                                                         CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
                                                                                                                                                                                                                                                                                                                                                              TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT 4385
GTCGTGCTTCTTTCCATTGTTAGTA 4529
                                                                                                                 CCATCCTTGACCATCT - CAACTGGGTCTTTGTGGTCATCTTTTACGTTAGAATGTCTCATC
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WLAPILABEEDDVEFSGEDNAQRITQPEBEDQAYELHQEKKEFISQRVQSVEIDMESED
EPHLTIQDPRKKSDVTSILSECSTIDLODGFGWLPENVPKKQPERCLPKGFGCCFPCC
SVDKRKPPWVIWMNLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVHLENQPKIQE
LLNCTDIIFTHIFILENVLKWVAFGFGKFTSAWCLDDFIIVTSVTTLINLMELKSF
RTLRALRPHALSQPEKKVVVNALIGAIPAILNVLLVCLIFHLVFCIIGAYFFSKFF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLSIVSTMISTLENQEHIPPPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
PSLEVISLLLFLIMFIYAILGMNWFSKVURESGIDDIRWKTFASSMLCLFQISTSAG
WDSLLSPMLRSKESCNSSENGHLFGJATSYFVSYIISFLIVVNMYIAVILENEVRIA
TEESEDPLGEDDFDIFYEVWEKFDPBATQFIKYSALSDFADALPEPLRVAKPNKYQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
QDIFMTEEQKKYYNAMKKLGSKKPQKFIPRPLNKCQGLVFDIVTSQIFDIIIISLIIL
NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGWNLFDCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLKII ALDPYHYFRRGWNI FDS I VALLSFADVMNCVLQKRSWFFLRSFRVLRVFKLAK
SWPTLNTLI KI IGNS VCALGNLTVVLVI VI FI FSVYGMQLFGRSFNSQKSFKLCNPTG
PTVSCLRHWINGDFWHSFLVVFRILGCEMI ENNMECMQBANASSSLCVI VFILI TVI
KLVVLNLFI ALLLNSFSNEERNGNLEGEARKTKVQLALDRFRRAFCFVRHTLEHFCHK
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HFDEHGDPLQRQRALSAVSILTITMKEQEKSQEPCLPCGENLASKYLVMNCCPQWLCV
KKVLRTVMTDPFTELAITICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIFIAEM
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQQLLKEEKEALVAMGIDRSSLTSLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKRIIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPLRTFRVFRALKAISVVSRLKVIVGALLRSVKKLVNVIILTFFCLSIFALVGQQLFM
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="AAF24976.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="voltage-gated sodium channel alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="SCN12A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          map="3p21.3-p23"
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chromosome="3"
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93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 163.4; DB 9
Pred. No. 3.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 6528;
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TITLE
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AUTHORS
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AC117294
LOCUS
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                                                                                                                                                                                                      Cardenas, V., Charter, K., Chen, C., Coyle, M., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cokvrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Dunn, A., Durbin, K., Daval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagy, M., Forbes, L., Foster, M., Garza, M., Gabisi, A., Gaita, R., Gardia, A., Garrer, T., Garza, M., Gebregorgis, B., Geer, K., Gill, R., Grady, M., Gurrer, W., Guvrara, W., Gunarathe, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havis, S., Hidaun, S.L., Hodgson, A., Hoples, M., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, A., Lu, W., Liu, Y., Lundon, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., Lundon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Lundon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Lundon, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Mahindartene, M., Mahnoud, M., Malloy, K., Mangum, A., Maheshwari, M., Martin, K., Martin, R., Martinez, E., Mangum, A., Mangum, B., Morris, S., Munidasa, M., Murphy, M., Nait, L., Peasternak, S., Peull, H., Perez, A., Perez, L., Peankoth, C., Pasternak, S., Peull, H., Perez, A., Perez, M., Norris, S., Riggs, F., Reilly, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
                                  Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1;
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Rattus norvegicus clone CH230-251M17, WORKING DRAFT SEQUENCE, 2
                                                                                                                                             Unpublished
                                                                                                                                                                                       Direct Submission
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                                                                                                          (bases 1 to 203255)
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REFERENCE

Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 203255)

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                       Matches
                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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On Oct 10, 2002 this sequence version replaced gi:21745888.
On Oct 10, 2002 this sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
73 CTAAACCATGATTGGCTTGATGGCCTAAATATACAACCCAACCCCAAAGCCATGGAATCCA 132
                                                                                       243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat Genome Sequencing Consortium
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: CH230-251M17
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 186626 bases at least Q40
Consensus quality: 188678 bases at least Q20
Consensus quality: 189877 bases at least Q20
Estimated insert size: 191689; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: GTMJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201993
                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig" complement(199245. .200177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201992: contig of 201992 bp in length 202092: gap of unknown length 3 203255: contig of 1163 bp in length. Location/Qualifiers
                                                                                                                                                                                                                             end_sequence:RXABQ81TJ'
                                                                                                                                                                                                                                                                                       /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                             site:Mbo]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="CH230-251M17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .203255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 938
                                                                                                                                                                                                                                                                                                                                                                                                   sequence:RXABQ81TV"
33. .30271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="genomic DNA"
_xref="taxon:10116"
                                                                                                           23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  College of Medicine
                                                                                    Score 134.8; I
Pred. No. 2.1e-
0; Mismatches
                                                                                       ٥,
                                                                                                                    2.1e-22;
                                                                                                                                        DB 2;
                                                                                       122;
                                                                                                                                           Length 203255;
                                                                                       Indels
                                                                                       5; Gaps
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                   RS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Badwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Badwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Beryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checkan, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Depar, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duvah, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggy, N., Forbes, L., Fostetr, M., Fostetr, P., Fernandez, S., Finley, M., Garia, A., Garner, T., Garza, M., Gebregocrgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gurratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Karapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowar, C., Kowar, C., Liu, J., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., Loho, H., Levan, J., Lewis, L., Li, Z., Liu, J., Mahmoud, M., Malloy, K., Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahiney, S., McLeod, M.P., McLeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4498 CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA 4555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4854 AAAGTTGCCA 4863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 GAAGTTGCTA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC127824 210800 bp DNA linear HTG 20-N
Rattus norvegicus clone CH230-51503, WORKING DRAFT SEQUENCE,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M.
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATAAACCCTAAAGATAATCA--TTTGGAAGTGTATCAAGGGTTTCCACAAAGCAACAGA 4793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGAAAA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGTTCTTTCTATCATTAGTAAAGTAAAACCAGTAGCCAGGACTTTCCAGGAAAGGCAGA 4735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGACTTTAAGAACCAGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCAAGTGTA-CTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACTGG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 210800)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                     Murphy, M., Nair, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG 20-NOV-2002
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Savery, G., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Taylor, C., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walls, R., Warren, R., Weden, H., Worley, K., Williams, G., Willson, R., Willey, R., Wooden, H., Worley, K., Willams, G., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23196353.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 210800)

Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329
Consensus quality: 177120 bases at least Q40
Consensus quality: 179072 bases at least Q30
Consensus quality: 180314 bases at least Q20
Estimated insert size: 179188; sum-of-contigs estimation
    208133
208233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GXXU Center clone name: CH230-51503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
208132: contig of 208132 bp in length 208232: gap of unknown length 209538: contig of 1306 bp in length
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ACCESSION VERSION KEYWORDS

> AC127215 AC127215.4 GI:24940804

ORGANISM

HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS

JOURNAL

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COMMENT

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clone_end:T7"
20214I .203014
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202181. .202273
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/mol_type="genomic DNA"
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                                      243048 bp
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.

Direct Submission

Submitted (14-UUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 243048)
                                                                                               Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23673556.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
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Anyalebechi, V., Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                          in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 243048)
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H., Alsbrooks, S.
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and separated
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18587 CATĀAACCCTĀĀĀGATAĀTCA--TTTGGĀĀĀGTGTATCAAGGGTTTCCACAAAGCAACAGA 18530

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_di
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence.
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GTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGAAAA
                                                                    GTGGTTCTTTCTATCATTAGTAAGTAAAACCAGTAGCCAGGACTTTCCAGGAAAGGCAGA
                                                                                                        GTGCTTCTTTCCATTGTTAAGTAAAATCAGCAGTCAGAGGGACTTTAAGAACCAGAA
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242020
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Assembly program: Phrap; version 0.990329
Consensus quality: 229285 bases at least Q40
Consensus quality: 231657 bases at least Q30
Consensus quality: 23138 bases at least Q20
Estimated insert size: 236807; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GDUK
Center clone name: CH230-10N16
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Contact: hgsc-help@bcm.tmc.edu
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clone_end:Sp6
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 134.8; DB Pred. No. 2e-22;
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Title:
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Aat77803	Ada50143	Abx12402	Aaf57009	Aa166959	Aat77804	Aax60243	Aaq81328	Aaq05831	Ab142420	Aa142751	Aaa93791	Adb78639	Adb78645	Abt 42021	Aav58423	Aav58419	Aav58421	Aav58420	Aav58422	Aax60872	Ada50151
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## ALIGNMENTS

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                                                                                        AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
                                                             Sequence 585 BP; 181 A; 117 C; 112 G; 175 T; 0 U; 0 Other;
                                                                                                                                                                                                                            Mammalian sodium channel protein for treating pain and hypersensitivity.
                                                                                                                                                                                                                                                             WPI; 1999-562112/47.
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                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                            Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; human nervous system; chromosome 3p23-21.3; excitatory cell; drug development; familial hyperglycaemia; QT extending syndrome
                                                                                                                                                                                                                                                                                                                                                                          AAL42750 standard;
                                        23-MAY-2000; 2000JP-00152085.
                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                        (first entry)
              SCI & TECHNOLOGY CORP
                                                                                                                                                                 Location/Qualifiers 200. .4534
                                                                                                                                          /product= "Human sodium channel subunit SCN12A-s"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present CDNA sequence encodes the human SCN12A-s sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 55-70; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5728 BP; 1637 A; 1241 C; 1199 G; 1650 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGACTCAGAAGTTTTTGTGGTGGTAACCTGATTT
                              ATGACTCAGAAGTTTTTGTGGTGGTAGAAAATTT 584
                                                                  CTGAAATAGAGTTCAATAATCATGCAGCTAATGTATTCAATGGAAATAGACAAAATTAAA
                                                                                      CTGAAATAGAGTTCAATAATCATGCAGCTAATGTATTCAATGGAAAATAGACAAAAATTAAA
                                                                                                                                     GGGAAGTTGCTAGGAGATA-----GAGAGTAATTTCTGTTCCCTTAACTCACTACACAA 4738
                                                                                                                                                         GGGAAGTTGCTAGGAGATAGGAGGCGGTAAATTTCTGGTTCCCCTTAACTCACTACACAA 489
                                                                                                                                                                                                          AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT
                                                                                                                                                                                                                                        AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT 429
                                                                                                                                                                                                                                                                           GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTCGTTCAAACTATCCACAAAGCAGA
                                                                                                                                                                                                                                                                                                           GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGA 369
                                                                                                                                                                                                                                                                                                                                               GTCGTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGACTTTAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                 GTCGTGCTTCTTTCCATTGTTAGTAAGTAAATCAGCAGTCAGAGGGACTTTAAGAACCA
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93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 425.8; DB 6; Length Pred. No. 3.4e-107; O; Mismatches 27; Indels
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4833
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Human

sodium channel NaN cDNA

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                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches | 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sodium channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia; hyperexcitability; analgesic; vaccine; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dib-Hajj S, Waxman SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-2000; 2000WO-US019342
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                                                                                                                                                                                                                                                                                                                                           Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other.
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                                                                 4276
                                                                                                                                                                                                         4158 TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT
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| 192; Conserv
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                                                                                       CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                  GTCGTGCTTCTTTCCATTGTTAGTA 274
                                                                                                                                      CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                                                                                                                                                                                               TACCTAAACCATGATTGGCTTGATGGCCTAAATATACAACCCAACCCCAAAGCCCATGGAAT
GTCGTGCTTCTTTCCATTGTTAGTA 4360
                                                                 Conservative
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                                                                                                                                                                                                                                                                                       27.9%;
                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                          Score 163.4; DB 4
Pred. No. 1.1e-34;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                           DB 4; Length 5860;
                                                                                                                                                                                                                                                                            11; Indels
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Matches 192;

Query Match Best Local Similarity

27.9%; ilarity 93.7%; Conservative

0,

Score 163.4; DB 9 Pred. No. 1.1e-34; 0; Mismatches 11

Indels Length 5860;

2

Gaps

2

DB 9;

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The present invention describes an expression vector comprising a nucleic cold sequence that encodes a mammalian Na v 1 9 sodium channel protein or clis fragment, and producing a sodium current when transfected in a cell. Cl Also described; (1) a recombinant cell comprising the plasmid selected comprising the cell or cell line that produces a Na v 1.9 composed comprising the cell or cell line that produces a Na v 1.9 composed cell that has been transfected with the expression vector; and (b) culturing the cell comprising the cell or cell that has been transfected with the expression of Na v 1.9 sodium channel protein comprising the cell or cell line produced by the method of composing the cell or cell line produced by the method to the agent; and cell by: (a) capable of modulating sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents considered in the expression and the name of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Na v 1.9 sodium channel protein encoding cDNA SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD32193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron
Sequence 5860 BP; 1628 A; 1313 C; 1293 G; 1626 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3; 125pp; English.
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                                                 is used
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                                                 in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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/product= "Na v 1.9 sodium channel protein'
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RESULT 5
AAL42749
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XX AAL4
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XX Huma
XX Homc
XX FT CDS
FT 
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                                                                                                         The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p32-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit proteins are useful for treating diseases such as familial subunit prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodium channel alpha subunits SCN12A and SCN8A of human nervous system together with splicing variants, useful in studying physiological mechanism relating to excitatory cells and in drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; human nervous system; chromosome 3p23-21.3; excitatory cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human sodium channel subunit SCN12A coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL42749 standard;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2000; 2000JP-00152085
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                                                                             present cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-393394/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 29-46; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
    B₽;
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1842 A; 1446 C; 1410 G;
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1830 T; 0 U; 0 Other;
                                                                                 SCN12A
                                                                                 sodium channel subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4275
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Query Match Best Local Similarity

27.9%; 93.7%;

Score 163.4; DB 6; Pred. No. 1.2e-34;

Length 6528

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RRESULT 6
AAX87620
IID AAX87
AAX876
AC AAX8
AC
                       This is the nucleotide sequence of a partial cDNA clone which codes for a contion (see AAY06596) of human NAN, a previously unidentified voltage cated sodium channel protein that is preferentially expressed in dorsal croot ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NAN channel cDNA was obtained from human DRG tissue cDNA by PCR amplification (see also AAX87620-22). Rat, mouse and human CMAN nucleic acids (see AAX8760-02) and polypetides (see AAX06596-98). The invention also includes expression vectors and ctransformed host cells, methods for identifying tissues and cells that cativity or NAN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and typerexcitability phenomena. The preferential expression of NAN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other concerns calls in the brain and spinal cord. The gene is named SCNIla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acids encoding sodium channels, used to develop products for treating acute or chronic pain or hyperexcitability
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20-NOV-1998;
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a; hyperexcitability; therapy; SCN11a gene; ss.
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ARESULT 7
AAF301AF 101 AAF31 11D AAF3 11D AAF3 12AF3 1
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              The present sequence is that of a partial cDNA for a novel human tetrodoctoxin resistant sodium channel, termed NaN (see AAB20125). The cDNA was isolated from a human dorsal root ganglia tissue cDNA library by PCR amplification (see also AAF30122-23). A full-length seeyence is given in AAF30101. Human NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory, neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF30104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF30104 standard; cDNA; 3701 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperexcitability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PSDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               channel; NaN; human; tetrodotoxin resistant; pain; paraesthesia;
hyperexcitability phenomena in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                             4; Fig 8A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3638 BP; 1027 A; 793 C; 801 G; 1016 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00354147
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1. .3699
/*tag= a
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NaN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
  human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 8
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Best Local Sim
Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            administering an agent that alters sodium current flow through NaN channels, or which modulates transcription or translation of NaN mRNA, dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used gene therapy to correct disorders associated with decreased sodium channel expression or (antisense) to down-regulate NaN expression, in diagnosis of disease, and in the recombinant production of NaN
                                                                                                                                                                                                                                                                                                                                                  Sodium channel; NaN; Scnlla; mouse; tetrodotoxin resistant; paraesthesia; hyperexcitability; analgesic; vaccine; gene tl
                                                                                 P-PSDB;
                                                                                         WPI; 2001-103147/11.
                                                                                                             Dib-Hajj S,
                                                                                                                                                                                              25-JAN-2001
                                                                                                                                                                                                                                              polyA_site
                                                                                                                                                                                                                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                 Mouse sodium channel NaN cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAF30103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3701 BP; 1043 A; 807 C; 820 G; 1030 T; 0
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                                                                                                                                  (UYYA ) UNIV YALE.
                                                                                                                                                     16-JUL-1999;
                                                                                                                                                                         14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF30103 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TACCTABACCATGATTGGCTTGATGGCCTABATATACAACCAACCCCABAGCCATGGAAT
                                                                                  AAB20124.
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                                                                                                               Waxman
                                                                                                                                                                         2000WO-US019342
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5800. F
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/*tag= c
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92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 131.4;
Pred. No. 6.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3701;
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Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.

The present sequence is that of cDNA encoding a novel

mouse tetrodotoxin

Example 3; Fig 7A; 162pp; English

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RESULT 9
ADD32195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC resistant sodium channel, termed NaN (see AAB20124). The CDNA was CS isolated from trigeminal ganglia cDNA using primers (see AAB30120-21) CC based on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN CC (see AAB20121). The gene encoding NaN, termed Scnila, is located on mouse CC chromosome 9. NaN belongs to the a-subduit voltage-gated sodium channel CC protein family and produces a TTX- subdium current. Such channels CC underlie the generation and propagation of impulses in excitable cells CC such as neurons and muscle fibres. Preferential expression of NaN on CC sensory neurons innervating the body (dorsal root ganglia) and the face CC (trigeminal ganglia), but not on other neurons, makes it a very useful CC target for diagnostic and/or therapeutic uses in relation to acute and/or CC chonic pain pathologies. A claimed method of treating pain, paraesthesia CC and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN CC channels, or which modulates transcription or translation of NaN mRNA, in CC dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in CC channel expression or (antisense) to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN
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Best Local (
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                                                    20-MAR-2002; 2002US-0365550P
                                                                                                         20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Na v 1.9 sodium channel protein encoding cDNA SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD32195;
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(TRAN-) TRANSMOLECULAR INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCTTTCCATCATTAGTA 4291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGGTGGTCGTG
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                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                /*tag=  a
/product= "Na v 1.9 sodium channel protein|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%;
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Pred. No. 9.4e-21;
0; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 1535 T; 0 U; 1 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
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Rattus norvegicus

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RESULT 10
ADD32209
ID ADD32
XX
AC ADD32
XX
DT 15-JA
XX
DE Rat N
XX
Expre
KW expre
KW sodiu
XX
OS Rattu
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; where an alteration in the level of sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a mouse Na v 1.9 sodium channel protein, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonda MA,
                                                                    expression vector; Na v 1.9 sodium channel protein;
                                                                                                        Rat Na v 1.9 sodium channel protein encoding cDNA SEQ
                                                                                                                                           15-JAN-2004
                                                                                                                                                                              ADD32209;
                                                                                                                                                                                                                  ADD32209 standard; cDNA; 5298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5822 BP; 1499 A; 1425 C; 1362 G; 1535 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present acid sequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                  sodium channel protein; dorsal root ganglion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its fragment, and producing a sodium current when transfected in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                         4273
                                                                                                                                                                                                                                                                                                                                                                              4213
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4095
                                                                                                                                                                                                                                                                                                                                                                                                               196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes an expression vector comprising a nucleic sequence that encodes a mammalian Na v 1.9 sodium channel protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGATATTCTCAACATAGTCTTCGTGGTCATCTTTACCGTAGAGTGTCTCATCAAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACATGATTATCATGATGGCTGAATCTGAAGGCCAGCCC--AACGAAGTGAAGAAAATC 4152
                                                                                                                                                                                                                                                                                                                             CTTCTTTCCATTGTTAGTA 274
                                                                                                                                                                                                                                                                                                         GTTCTTTCCATCATTAGTA 4291
                                                                                                                                                                                                                                                                                                                                                                                TTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                    TTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCAACAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greenwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 113; DB 9;
Pred. No. 9.4e-21;
0; Mismatches 45
                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                     neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                     rat; gene;
                                                                                                           ij
                                                                                                           NO:19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135
                                                                                                                                                                                                                                                                                                                                                                                                                   255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Nav1.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; SEQ ID NO 19; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003; 2003WO-US008611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003080570-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its fragment, and producing a sodium current when transfected in
                                       4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-876895/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                       153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMOLECULAR INC.
                                                                   5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other;
   GTGCTTCTTTCCATTGTTAGTA
                                         GTCTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTC
                                                                                                                   ACCTTTGATATCCTCAACATAGCCTTCGTGGTCATCTTTACCATAGAGTGTCTCATCAAA
                                                                                                                                       TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAA
                                                                                                                                                                                             CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA
                                                                                                                                                                                                                               CTARACCATGATTGGCTTGATGGCCTARATATACARCCARCCCCARAGCCATGGAATCCA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenwood JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Na v 1.9
                                                                                                                                                                                                                                                                                       19.3%;
75.7%;
                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                     Score 112.8; DB
Pred. No. 1e-20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sodium channel protein"
                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                           Length 5298;
                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a cell.
                                         4248
                                                                                                                   4188
                                                                                                                                                                                             4128
                                                                               252
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RESULT

AAX87600
ID AAX8
XX
AC AAX8
XX
DT 26-C

AAX87600;

26-OCT-1999

(first entry)

AAX87600 standard;

CDNA; 5875

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                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 153;
                                                                                                                                                                                                                                                                                                               The present sequence encodes a type 5 sodium channel protein designated PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                                                                                                                                                                                                                                                     Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stabilised cDNA encoding type 5 sodium channel protein designated PNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX60244 standard; cDNA; 5334
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Fig 5A-E; 90pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated DNA encoding sodium channel of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-315739/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2771103-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropathic pain; migraine; headache; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                      4212
4272
                                                                                                               4152 ACCTTTGATATCCTCAACATAGCCTTCGTGGTCATCTTTACCATAGAGTGTCTCATCAAA
                                                                                                                                                                        4094 CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA
                                                                                 133 ТССТТВАССАТСТССААСТВЕВТСТТТВТВЕТСАТСТТТАСВТТАВЛАТВТСТСАТСЛАА 192
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                 CTARACCATGATTGGCTTGATGGCCTARATATACARCCARCCCCARAGCCATGGARTCCA 132
Greenreitretareatraera 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS,
                         GTGCTTCTTTCCATTGTTAGTA 274
                                                       GTCTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTC
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fish LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0066225P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98FR-00014551.
                                                                                                                                                                                                                                             19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Khare
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                              Score 112.8; DB Pred. No. 1e-20; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous
                                                                                                                                                                                                                               47;
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                                                                                                                                                                                                                                                          Length 5334;
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                                                                                                                                                                                                                               Gaps
                                                         4271
                                                                                                                4211
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                                                                                     252
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Rat

sodium channel NaN

CDNA.

paraesthesia;

sodium channel; ion transport; rat; dorsal root ganglia; pain; esthesia; hyperexcitability; therapy; Scnlla gene; ss.

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                                                                                                                                                                                                                               This is the nucleotide sequence of an isolated nucleic acid which encodes the rat NaN channel (see AAY06596), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from Sprague-Dawley rat DRG cDNA by PCR and RACE amplification (see also AAX87603-17). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see CC AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN CC channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in Sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord. The NaN gene has been named
                                                                                                                          Matches 153;
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                      Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dib-Hajj S, Waxman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1998;
20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phenomena.
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                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-479168/40
                            133
                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY06596
                            TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAA 192
ACCTTTGATATCCTCAACATAGCCTTCGTGGTCATCTTTACCATAGAGTGTCTCATCAAA
                                                           CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acids encoding sodium channels, used to develop treating acute or chronic pain or hyperexcitability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0072990P.
98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US002008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
5551. 5600
/*tag= b
/*tag= b
/*tag= b
/note= "these bases represent nucleotides missing from
/note equence given in Fig 1 of the specification. The
nucleotides are included to maintain the nucleotide
numbering given in the specification for this DNA
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41. .5338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91pp; English
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                                                                                                                                      19.3%;
                                                                                                                       0;
                                                                                                                                      Score 112.8;
Pred. No. 1.1
                                                                                                                          Mismatches
                                                                                                                                         .1e-20;
                                                                                                                                                      DB 2;
                                                                                                                        47;
                                                                                                                          Indels
                                                                                                                                                     Length 5875;
                                                                                                                        2
                                                                                                                       Gaps
                                                           4168
                                                                                           132
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AAF30102
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                                                     cc sodium channel proteins) and NaN-specific primers (see also AAF30105-19), cc and RACE amplification. The open reading frame shows 73% similarity to the human NaN sequence (see AAF30101). NaN belongs to the a subunit cc the human NaN sequence (see AAF30101). NaN belongs to the a subunit cc current. Such channel protein family and produces a TTX-R sodium cc current. Such channels underlie the generation and propagation of cc impulses in excitable cells such as neurons and muscle fibres. Cc referential expression of NaN on sensory neurons innervating the body constant root ganglia) and the face (trigeminal ganglia), but not on other concerns, makes it a very useful target for diagnostic and/or therapeutic cuses in relation to acute and/or chronic pain pathologies. A claimed cc method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters codium current flow through NaN channels, or which modulates codium current flow through NaN mannels, or which modulates trigeminal neurons. NaN nucleic acids are used in gene therapy to correct construction of the negulate NaN expression, in the diagnosis of disease, cc and in the recombinant production of NaN polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of cDNA encoding a novel rat tetrodotoxin resistant sodium channel, termed NAN (see AAB20122). The cDNA was isolated from a dorsal root ganglia tissue cDNA library by PCR amplification using generic primers (from conserved resions of a-subunit sodium channel proteins) and NaN-specific primers (see also AAF30105-19),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 162pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-103147/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-2000; 2000WO-US019342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200105831-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat sodium channel NaN cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF30102 standard; cDNA; 5875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYYA ) UNIV YALE.
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Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T; 0 U; 2 Other;

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RESULT 14
ARAZ1480
ID 21A221
XX AAZ21
XX AAZ21
XX AAZ21
XX AAZ21
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Best Local S
Matches 153
  Query Match
Best Local S
Matches 153
                                                                                                                             The present sequence encodes rat sensory neurone specific 2a (SNS-2a). SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                           Mammalian sodium channel protein for treating
                                                                                                                                                                                                                                                                                                                                                                                                                        Grose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sensory neurone specific 2a; SNS-2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat sensory
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                                                                                      Sequence 5897
                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-562112/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1999.
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    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    DT, Hick CA,
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                                                                                                                                                                                                                                                               4; Page 52-58; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                        AAY41668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCTTCTTTCCATTGTTAGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTTTGCTTTGAGGCAACACTACTTCACCAATGGCTGGAACTTATTTGATTGTGTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA
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    Conservative
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                                                                                      BP; 1474 A; 1471 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB000838
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                    19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Tate
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    0
Score 112.8; DB 2
Pred. No. 1.1e-20;
0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112.8; DB 4
Pred. No. 1.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide sequence
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                                                                                      1435 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sodium channel protein;
                                         DB 2;
                                                                                      1517 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                        pain
                                                                                      0 U; 0 Other;
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    Indels
                                         Length 5897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                           hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5875;
                                                                                                                                  hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
2.
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    Gaps
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RESULT 15
ADB52929
ID ADB52929
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XX ADB52
XX VOALE
C C C The
ADB52929
AC ADB52
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19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                    04-SEP-
28-JAN-
                                                                                                                                                                                                                                                                                                                                                                              09-JUL-2002;
09-JUL-2002;
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08-APR-2002;
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Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox

2003-731472/69

Claim

44; SEQ

ID NO

3471; 874pp;

English

for

determining whether

The present invention describes a method

밁 Ś 밁 Ş 밁 Query Match Best Local Similarity Matches 153; Conserv compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention. Sequence 5905 BP; 1476 A; 1471 C; 1439 G; 1519 T; 0 U; 0 Other; 4300 4180 ACCTTTGATATCCTCAACATAGCCTTCGTGGTCATCTTTACCATAGAGTGTCTCATCAAA 4239 4122 CTTAAATATGATTATCATGATGGCTGAATCTGCCGACCAGCCC--AAAGATGTGAAGAAA 4179 253 133 TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTTACGTTAGAATGTCTCATCAAA 192 GTGCTTCTTTCCATTGTTAGTA 274 GTGGTTCTTTCTATCATTAGTA 4321 19.3%; Score 112.8; DB 9; ilarity 75.7%; Pred. No. 1.1e-20; Conservative 0; Mismatches 47; Length 5905; Indels 2 Gaps

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Search completed: March 22, 2004, 16:13:20 Job time: 425.441 secs

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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5 US-10-202-824-7
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                                                                                              Matches 192;
                                                                                                                   Query Match
Best Local Similarity
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REBERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/10/388,470

CURRENT FILING DATE: 2003-03-17

PRIOR APPLICATION NUMBER: US/09/354,147C

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR FILING DATE: 1998-01-29

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR FILING DATE: 1998-11-20

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: PCT/US99/02008

PRIOR FILING DATE: 1999-01-29

NUMBER: OF SEQ ID NOS: 44
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APPLICANT: Waxman,
                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                                                                                          LENGTH: 5860
TYPE: DNA
4158 TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT 4216
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0; Mismatches 11
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CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR PRILING DATE: 1999-07-16
PRIOR PPLICATION NUMBER: US 60/072,990
PRIOR PPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
Sequence 4, Application US/10388470 Publication No. US20030228662A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 44
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APPLICANT: Waxman, Stephen G
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(3699)
OTHER INFORMATION: partial human NaN cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3701
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                      3649
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                                                                                                                                                                                                                                                                                         3531 TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT
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ilarity 92.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
ITILE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR APPLICATION NUMBER: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
ROOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44-2
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US-10-388-470-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (5804)
OTHER INFORMATION: cDNA sequence of mouse NaN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (19)..(5313)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4213
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Pred. No. 1.4e-20;
0; Mismatches 45;
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SEQ ID NO 1 LENGTH: 5875

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Sequence 104, Application US/10220120
Publication No. US20040048253A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
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Best Local S
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LOCATION: (1996)..(4042)
OTHER INFORMATION: n = a or c
OTHER INFORMATION: 652 is Leu;
OTHER INFORMATION: or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus FEATURE:
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                                             YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGTTCTTTCTATCATTAGTA 4310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGCTTCTTTCCATTGTTAGTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAHL, Tam C.
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                                                                                                                                                                                                                                                                                 AMSHEY, Steram
NAHL, Christopher R.
                                                                                                                     RUSSO, Frank D.
STOCKDREHER, Theresa
                                                                                                                                     ROSEN, Bruce H. RUSSO, Frank D.
                                                                                                                                                               LIU, Tommy F. ROSEBERRY, Ann M.
                                                                                                                                                                                                            GREENAWALT, Lila B.
                                                                                                                                                                                                                             FONG,
                                                                                                                                                                                                                                      DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
                                                                                                                                                                                                                                                               DANIELS,
                                                                                                                                                                                                                                                                                                                         CHALUP, Michael S.
CHANG, Simon C.
CHEN, Alice
                                                                                                                                                                                                                                                                                                                                                                   SHAH, Purvi
                                                                                                                                                                                                                                                                                                                                                                                        PANZER, Scott R
SPIRO, Peter A.
             HODGSON, David M.
                           COHEN,
                                       CHEN, Wensheng
                                                                                                  WRIGHT, Rachel J.
                                                                                                             DAFFO, Abel
                                                                                                                                                                                       JONES, Anissa L.
                                                                                                                                                                                                     HILLMAN, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                            BANVILLE,
LINCOLN, Stephen E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                  Steven A.
                        Howard J.
                                                                                                                                                                                                                                                                                                                                                                                                     Scott R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.3%;
75.7%;
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Pred. No. 1.6e-20;
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amino acid
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US-10-202-824-3

Sequence 3, Application US/10202824
Publication No. US20030176648A1
GENERAL INFORMATION:

APPLICANT: Wood, John N.
Akopian, Armen N.
TITLE OF INVENTION: Ion Channel

NUMBER OF SEQUENCES:

ZIP: 19850 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

STATE: Delaware COUNTRY: USA

CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals
STREFT: 1800 Concord Pike, P.O. Bo
CITY: Wilmington

Box 15437

RESULT 6

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FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,776; 60/184,777; 60/184,773; 60/184,776; 60/184,771; 60/184,771; 60/184,813; 60/184,773; 60/184,776; 60/184,771; 60/184,813; 60/184,897; 60/184,841; 60/184,772; 60/185,213; 60/184,837; 60/184,863; 60/205,221; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/204,815; 60/205,328; 60/205,321; 60/204,525; 60/205,324; 60/205,285; 60/205,285; 60/205,287; 60/204,525; 60/205,286; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287; 60/205,287
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; LOCATION: 6797, 7046, 72:
; OTHER INFORMATION: a, t,
US-10-220-120-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8530
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER_INFORMATION: Incyt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
4919
                                                                                                                                             4859
                                                                                                                                                                                                                                                                                                  4801
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4741 AGACAAGCTTTTGACATCACCATCATGGTCCTCATCTGCCTAAACATGGTTCACCATGAT
                                                                                                                                                                                                                154 GTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCTTTGCTTTGAGGCAATAC 213
                                                                                                                                                                                                                                                                                                                                                                         34 AGCCCAGGCAGTCTTTTCGACATCATCATAAGCTCATACCTAAACCATGATTGGCTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%;
Similarity 62.3%;
                                                                  TACTTCACCAATGGCTGGAATTTATTTGACTGTGGTGGTCGTGCTTCTTTCCATTGTTAG 272
TACTTCACAAATGGCTGGAATGTGTTTGACTTCATTGTGGTGGTTCTCTCCATTGCGAG 4977
                                                                                                                                                                                                                                                                                          GGTGGAGACTGATGACCAAAGTGAA--GAAAAGACGAAAATTCTGGGCAAAATCAACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NOS: 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.2; DB 12
Pred. No. 1.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
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US-10-209-776-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10209776
Publication No. US20030096360A1
GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PattentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/209,776.
FILING DATE: 01-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-7466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 561..2126
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CLONED PERIPHERAL NERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Herman, Ronald C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAAATCT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGCAGAATCAACCAGTTCTTTGTGGCCGTCTTCACGGGCGAGTGTGATGAAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/669,656 FILING DATE: 24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/202,824 FILING DATE: 26-Jul-2002
                                                                                                                                                                                                                              ADDRESSEE: Syntex Corporation, Patent Department A2-200 STREET: 3401 Hillview Avenue P.O. Box 10850 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGTCCATTGGGAGT 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTTTCCATTGTTAGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                           COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Stephen G
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Pred. No. 9.
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CELL TYPE: Poripheral nerve
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-209-776-1
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Publication No. US20030176648A1
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/10/202,824

FILING DATE: 26-Jul-2002

CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals
STREET: 1800 Concord Pike, P.O. Box 15437
CITY: Wilmington
CITY: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Peries, Rohan
REGISTRATION NUMBER: 35,752
REFERENCE/DOCKET NUMBER: 28340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-852-1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/511,828
FILING DATE: <Unknown>
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4668
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ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4608 TCGCCCTGCGACAGTACTACTTCACCAACGGCTGGAACGTGTTCGACTTCATAGTGGTGA 4667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4548 TGGGCAGAATCAACCAGTTCTTTGTGGCCGTCTTCACGGGCGAGTGTGTGATGAAGATGT 4607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 TIGCTITGAGGCAATACTACCTACCAATGGCTGGAATTTATTTGACTGTGTGGTCGTGC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCATAAATCT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.9%; 1 Similarity 69.3%; 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          John N.
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Pred. No. 1.6e-08;
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Query Match
Best Local Similarity
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US-10-202-824-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10202824
Publication No. US20030176648A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (302) 886-7466
INFORMATION FOR SEQ ID NO: 1:
              INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6527 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                           REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-7466
                                                                                                                                                  APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4852 TCCTGTCCATTGGGAGT 4868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1732 TGGGCAGAATCAACCAGTTCTTTGTGGCCGTCTTCACGGCGAGTGTGTGATGAAGATGT
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTTTCCATTGTTAGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712
                                                                                                                                      REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1800 Con
CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 204..6077
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1800 Concord Pike, P.O. Box 15437
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Pred. No. 1.6e-08;
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                                                                                                                                                                                                                                                                                                                                   Version #1.25
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LOCATION: 204...

SEQUENCE DESCRIPTION:
US-10-202-824-5
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US-10-202-824-5
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Publication No. US20030176648A1
GENERAL INFORMATION:
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                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (302) 886-7466 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/202,824
FILING DATE: 26-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,656
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akopian, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
                                                                                  FEATURE:
                                                                                                 TOPOLOGY:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wood, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4792 TCGCCCTGCGACAGTACTACTTCACCAACGGCTGGAACGTGTTCGACTTCATAGTGGTGA 4851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                 LENGTH: 7052 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                        NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGTCCATTGGGAGT 4868
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Delaware
                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1800 Concord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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204..6077
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OO Concord Pike, P.O. Box 15437
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                                SEQ ID NO:
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Pred. No. 1.6e-08;
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patent No. US20020061524A1
GENERAL INFORMATION:
APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
                                                                                                                                                                           Sequence 1, Application US/09896994 Publication No. US20030074024A1
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Best Local
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LOCATION: (1)..(6048)
-09-840-125-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/840,125
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR PELICATION NUMBER: 60/147,488
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2323-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 6048
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            APPLICANT: Ken Stokes
APPLICANT: Ken Stokes
Jos e Morissette
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5317
                                                                                                                                                                                                                                                                                                       4797 CATCCTCCCATCGTGGGCA 4816
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96; Conserv
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                                                                                                                                                                                                                                                                                                                                                GCTTCTTTCCATTGTTAGTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGGCCAAGATCAACCTGCTCTTTGTGGCCATCTTCACAGGCGAGTGTATTGTCAAGCT 4736
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SPONDENCE ADDRESS:
ADDRESSEB: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024Alris
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Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69.6; DB 9;
Pred. No. 1.7e-08;
D; Mismatches 44;
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US-10-077-054-1
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                                                     US-10-077-054-1
                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 6091
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10077054 Publication No. US20030157600A1
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          Query Match
                                                                                                                                                                                                                                                        APPLICANT: Makielski, Jonathan C
APPLICANT: Ye, Bin
TITLE OF INVENTION: Sodium Channel Alpha Subunits
FILE REFERENCE: 960296.98032
CURRENT APPLICATION NUMBER: US/10/077,054
CURRENT FILING DATE: 2002-02-12
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 10
                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(6054)
                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                          TYPE: DNA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,994
FILING DATE: 02-Unl-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/514,907
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4797 CATCCTCTCCATCGTGGGCA 4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4737 GGCTGCCCTGCGCCACTACTTCACCAACAGCTGGAATATCTTCGACTTCGTGGTTGT 4796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 CTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAAT 194
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Similarity 68.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTCTTTCCATTGTTAGTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
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            11.9%;
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Pred. No. 1.7e-08;
            Score 69.6;
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            DB 14; Length 6091;
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Gaps

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US-10-101-510-617
Sequence 617, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
                                                    , NAME/KEY: modified_base
; LOCATION: (8167)
; OTHER INFORMATION: a, t,
US-10-101-510-617
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SEQ ID NO 617
LENGTH: 8490
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                           Query Match
  Matches
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CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
                                                                                                                  LOCATION: (7538)
OTHER INFORMATION: a,
                                                                                                                                                                   NAME/KEY: modified base LOCATION: (7477)..(7478) OTHER INFORMATION: a, t,
                                                                                                                                                                                                                      NAME/KEY: modified base LOCATION: (7300)...(7301) OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
LOCATION: (7286)
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LOCATION: (7227)
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LOCATION: (6774)
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  Local Similarity 68.6
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Score 69.6; DB 14;
Pred. No. 2.1e-08;
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Mismatches 44;
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                        Length 8490;
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Search completed: March 23, Job time: 363.296 Becs
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US-10-333-191-1
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                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (151)..(6198)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 2323-154-ÎI
CURRENT APPLICATION NUMBER: US/10/333,191
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/US01/22639
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,738
PRIOR FILING DATE: UNMBER: US 60/219,738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Keating, Mark T.
APPLICANT: Splawski, Igor
TITLE OF INVENTION: Common Polymorphism in
TITLE OF INVENTION: Arrhythmia
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(8491)
OTHER INFORMATION: n m.
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                                                              4947 CATCCTCTCCATCGTGGGCA 4966
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68.6%;
             2004, 05:15:03
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Pred. No. 2.1e-08;
0; Mismatches 44
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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585
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Copyright (c) 1993 - 2004 Compugen Ltd.
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m2_6/ptodata/2/pna/USO6_COMB.seq:*
m2_6/ptodata/2/pna/USO6_COMB.seq:*
m2_6/ptodata/2/pna/USO8_COMB.seq:*
m2_6/ptodata/2/pna/USO81_COMB.seq:*
m2_6/ptodata/2/pna/USO82_COMB.seq:*
m2_6/ptodata/2/pna/USO82_COMB.seq:*
m2_6/ptodata/2/pna/USO83_COMB.seq:*
m2_6/ptodata/2/pna/USO83_COMB.seq:*
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469 / cgm2_6/prodate/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

Length 585; Indels

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Gaps

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180

240 180 120

60

120

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APPLICANT: Glaxo Wellcome PLC
APPLICANT: Tate, Simon N
APPLICANT: Tate, Simon N
APPLICANT: Hicks, Caroline A
TITLE OF INVENTION: Ion Channels
FILE REFERENCE: PG3432
CURRENT APPLICATION NUMBER: US/09/646,224A
CURRENT FILLING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: GB 9805793.8
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-09-646-224A-16
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09646224A GENERAL INFORMATION:
  TYPE: DNA
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PCT-US03-08611-3
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US-10-388-470-41
US-00-516-609-317
US-00-516-609-317
US-00-770-175-8399
US-10-296-130-1
US-00-213-846-1412
PCT-US09-02008-6
PCT-US09-02008-6
PCT-US09-02008-4
PCT-US03-08611-5

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3 US-60-365-550-19
5 US-09-195-851-4
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US-10-001-187-49
US-10-70-235-13985
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US-60-453-135-2171
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Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 317, App
Sequence 8399, Appli
Sequence 1, Appli
Sequence 6, Appli
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Sequence 9, Appli
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Sequence 124, App
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Sequence 93, Appl
Sequence 49, Appl
Sequence 49, Appl
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Sequence 13985, A
Sequence 2171, Ap
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Sequence 1, Ap
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Sequence 3, A
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Appl.
                                                                                                                                                                                                          APPLICANT: The General Hospital Corporation doing bus APPLICANT: Hospital / Bayer AG ITILE OF INVENTION: Nucleotide sequences involved in FILE REFERENCE: LeA 35693 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT FILING DATE: 2003-05-09 PRIOR APPLICATION NUMBER: US 60/312,147 PRIOR FILLING DATE: 2001-08-14 PRIOR FILING DATE: 2001-08-14 PRIOR APPLICATION NUMBER: US 60/346,382 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR FILING DATE: 2001-11-01 PRIOR FILING DATE: 2001-11-26 NUMBER: US 60/333,347 PRIOR PRIOR PRIOR FILING DATE: 2001-11-26 NUMBER: US 60/333,347 PRIOR PRIO
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US-10-219-051B-910
S-910-10-219-051B-910
Sequence 910, Application US/10219051B
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                  SOFTWARE: Perl script SEQ ID NO 910
LENGTH: 5728
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(5728)
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FILE REFERENCE: 2002-1512A/WMC/00653

CURRENT APPLICATION NUMBER: US/10/296,130

CURRENT FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: PCT/JP00/04629

PRIOR APPLICATION NUMBER: JP2000-152085

PRIOR FILING DATE: 2000-05-23

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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Sequence 3, Application US/10296130
GENERAL INFORMATION:
APPLICANT: KANAZAWA, Ichiro
APPLICANT: GOTO, Jun
APPLICANT: JEONG, Seon-Yong
TITLE OF INVENTION: Human Sodium Channel SCN12A and
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Best Local Similarity
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: EMBL /
DATABASE ENTRY DATE: 2000-01-16.
                                                                  LENGTH: 5728
TYPE: DNA
ORGANISM: Homo sapiens
                             NAME/KEY: CDS
LOCATION: (200)..(4534)
                                                           FEATURE:
NAME/KEY: modified base
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Sequence 84151, Application US/60466412
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCADIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CLO01466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
CURRENT FILING DATE: 2003-04-30
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Best Local Similarity
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OTHER INFORMATION: n = a, g, c or t
PUBLICATION INFORMATION:
AUTHORS: Soen Yong Jeong et al.
TITLE: Identification of a Novel Human Voltage-Gated Sodium Channel
TITLE: Gene, SCN12A
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DATE: 2000-01-15
DATABASE ACCESSION NUMBER: GenBank AF150882
DATABASE ENTRY DATE: 2000-01-15
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Pred. No. 6e-106;
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NUMBER OF SEQ ID NOS: 429241 SOFTWARE: FastSEQ for Window SEQ ID NO 84151

Windows Version

LENGTH: 11

115159

ORGANISM: Homo sapiens

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APPLICANT: BONAZZI, VIVIEN
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN I
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000126
CURRENT APPLICATION NUMBER: US/60/162,357
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 1748
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 124
LENGTH: 614
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; NAME/KEY: misc feature
; LOCATION: (1)...(115159)
; OTHER INFORMATION: n = A,T,C
US-60-466-412-84151
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US-60-162-357-124/c
; Sequence 124, Application US/60162357
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                    TYPE: DNA
ORGANISM: Human
-60-162-357-124
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nilarity 93.2%;
Conservative
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                                                            64.9%;
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                                                  Score 379.4; DB 72;
Pred. No. 1.6e-93;
0; Mismatches 16;
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RESULT 6
US-60-163-080-93/c
Sequence 93, Application US/60163080
Sequence 93, Application US/60163080
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN INTITLE OF INVENTION: AND USES THEREOF
FILE REFRENCE: CL000136
CURRENT APPLICATION NUMBER: US/60/163,080
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 760
SOLTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 614
TYPE: DNA
ORGANISM: Human
US-60-163-080-93
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                CTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGAAAACTGGGCCAAGTGTA 386
                                                                                                                   GCAATACTACTTCACCAATGGCTGGAATTTATTTGACTGTGTGGTCGTGCTTCTTTCCAT
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Pred. No. 1.6e-93;
0; Mismatches 16;
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RESULT 8
US-09-364-7)31A-49
; Sequence 49, Application US/09364791A
; GENERAL IMFORMATION:
; APPLICANT: Robison, Kieth E.
; TITLE OF INVENTION: Novel Ion Channel Homologs
; FILE REFERENCE: 5800-42
; CURRENT APPLICATION NUMBER: US/09/364,791A
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 76
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; LOCATION: (0)...(0)
; OTHER INFORMATION: CALCIUM AND SODIUM CHANNELS
US-09-364-791-49
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CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/09364791
GENERAL INFORMATION:
APPLICANT: Robison, Kieth E.
TITLE OF INVENTION: Novel Ion Channel Homologs
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Best Local Similarity
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                          GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGA 375
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Sequence 49, Application US/10001187
GENERAL INFORMATION:
APPLICANT: Robison, Kieth E.
TITLE OF INVENTION: Novel Ion Channel Homologs
FILE REFERENCE: 5800-42
CURRENT APPLICATION NUMBER: US/10/001,187
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US/09/364,791
PRIOR APPLICATION NUMBER: US/09/364,791
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: CALCIUM AND SODIUM CHANNELS
US-09-364-791A-49
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US-10-001-187-49
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LENGTH: 435
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Best Local Similarity
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                               Match 54.2%; Local Similarity 96.1%;
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                                                                    AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT 429
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96.1%;
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                                                                                                                 0; Mismatches
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Pred. No. 2.5e-76;
                                                                                                                 Score 316.8; DB 43; Pred. No. 2.5e-76; 0; Mismatches 12;
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US-60-453-050-2171
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; ORGANISM: HUMAN
US-10-170-235-13985
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US-10-170-235-13985
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SEQ ID NO 2171
LENGTH: 5080
TYPE: DNA
                                     Sequence 2171, Application US/60453050

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US
FILE REFERENCE: CL001457
CURRENT EPLICATION NUMBER: US/60/453,050
CURRENT EPLICATION NUMBER: US/60/453,050
CURRENT ETLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 13985
LENGTH: 5080
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TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CL001380
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93.7%;
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Pred. No. 1.4e-33;
0; Mismatches 11;
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RESULT 13
US-60-466-412-2171
US-60-466-412-2171
; Sequence 2171, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olde
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION
; FILE REFERENCE: CL001466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INCOUDUA, OIGA
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-135-2171
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US-60-453-135-2171
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Best Local (
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93.7%;
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APPLICANT: Yale University
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Maxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in
FILE REFERENCE: 44574-5004-02-WO
CURRENT APPLICATION NUMBER: PCT/US00/19342
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/354,147
PRIOR APPLICATION NUMBER: US 09/354,147
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 44
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 5860
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PCT-US00-19342-41
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, LOCATION: (31)..(5403)
, OTHER INFORMATION: full length cDNA sequence for human NaN
PCT-US00-19342-41
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CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 429241
SOFTWARE: FBSUSEQ for Windows Version 4.0
SEQ ID NO 2171
LENGTH: 5080
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
-60-466-412-2171
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                      Local Similarity 93.7
les 192; Conservative
4276
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                                                                                                     CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
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                         CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                                                                                                       TATÉCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT
                                                                                                                                                                                                                        27.9%;
93.7%;
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                                                                                                                                                                                                     Score 163.4; Db 1;
Pred. No. 1.4e-33;
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                                                                                                                                                                                                                                           Length 5860;
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GTCGTGCTTCTTTCCATTGTTAGTA 274

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APPLICANT: GREENWOOD, John D
TITLE OF INVENTION: Recombinant Expression Ver
FILE REFERENCE: 51530-5007-WO
CURRENT APPLICATION NUMBER: PCT/US03/08611
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/365,550
PRIOR FILING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 5860
 Search completed: March 23, Job time: 4411.36 secs
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PCT-US03-08611-3
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Best Local Similarity 93.7%;
Matches 192; Conservative
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FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(54
OTHER INFORMATION:
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time : 4411.36 secs
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                                                                                           GTCGTGCTTCTTTCCATTGTTAGTA 274
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                 2004, 04:00:39
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Pred. No. 1.4e-33;
0; Mismatches 11;
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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score:
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seq length:
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Gapop 10.0 , Gapext 1.0
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585
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(cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
(cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
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(cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
(cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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         US-10-487-337-5

US-10-487-337-1

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US-60-548-091-267

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US-60-548-091-5582

US-60-548-091-5582

US-60-548-091-5582

US-10-796-280-6719

US-10-796-280-6751

US-10-796-280-6815

US-10-796-280-6845

US-10-796-280-6845

US-10-796-280-381

US-10-796-280-381

US-10-796-280-381

US-10-796-280-381

US-10-796-280-383

US-10-796-280-383

US-10-796-280-389

US-10-796-280-389
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         Sequence 1, Appli
Sequence 266, App
Sequence 268, App
Sequence 5562, Ap
Sequence 5566, App
Sequence 6719, Ap
Sequence 6713, Ap
Sequence 6815, Ap
Sequence 6873, App
Sequence 6873, App
Sequence 381, App
Sequence 382, App
Sequence 372, App
Sequence 382, App
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Sequence 5675, Ap
Sequence 1, Appli
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5.7	л • 7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5.8	5.8	5.9	5.9	6.0	6.0	6.1
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US-10-021-698A-898	US-10-796-280-12377	US-60-548-091-5581	US-10-796-280-6891	US-10-796-280-6863	US-10-796-280-6835	US-10-796-280-6803	US-10-796-280-6771	US-10-796-280-6739	US-10-796-280-6707	US-09-796-692B-8469	US-10-663-208A-10	US-10-646-301A-10	US-10-793-479-13604	US-09-554-151C-39	US-10-667-762-23	US-60-550-051-2987	US-09-969-034-1306	US-10-417-375A-12
	Seguence 12377;	Sequence 5581, A	Sequence 6891, A	Sequence 6863, A	Sequence 6835, Ap	Sequence 6803, Ap	Sequence 6771, Ap	Sequence 6739, Ap	Sequence 6707, Ap	•	Sequence 10, App	Sequence 10, App	Sequence 13604, i	Sequence 39, App.	Sequence 23, App.	Sequence 2987, Ap	Sequence 1306, Ap	Sequence 12, App.

## ALIGNMENTS

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                          Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                         LENGTH: 5874
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(5874)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
APPLICANT: LOUIS POON
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REFERENCE: 117-492 / N 86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT FILLING DATE: 2004-02-20
4643
                                                                             4583 TCGCTTTGAGGCAGTACTACTTCACAAATGGCTGGAATGTGTTTGACTTCATTGTGGTGG
                                                                                                                                                           4523 TGGGCAAAATCAACCAGTTCTTTGTGGCCGTCTTCACAGGCGAATGTGTCATGAAGATGT
                                     257
                                                                                                                 137 TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCT
                                                                                                                                                                                                                                                             Similarity
TTCTCTCCATTGCGAG 4658
                                   TTCTTTCCATTGTTAG 272
                                                                                                                                                                                                                                      13.9%; Score 81.6; DB 6; 75.0%; Pred. No. 1.3e-14; tive 0; Mismatches 34;
                                                                                                                                                                                                                                                                              Length 5874;
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RESULT 2 US-60-548-091-5675 ; Sequence 5675, Application US/60548091

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; LCGATION: (1)...(100374)
; OTHER INFORMATION: n = A,T,C or G,
US-60-548-091-5675
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CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5675
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 6524
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APPLICANT: CARGILL,
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
                                                                                Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOUIS POON
APPLICANT: John Nicholas WOOD
APPLICANT: Misbah MALIK-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REFERENCE: 117-492 / N.86242A GCW
CURRENT PEPLICATION NUMBER: US/10/487,337
CURRENT FILING DATE: 2004-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
APPLICANT: Louis POON
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (204)...(6074)
OTHER INFORMATION:
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                                                                                                   Local Similarity
4732 TGGGCAGAATCAACCAGTTCTTTGTGGCCGTCTTCACGGCCGAGTGTGTGATGAAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                    137 TGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCT 196
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GENETIC POLYMORPHISMS ASSOCIATED WITH
STROKE, METHODS OF DETECTION AND USES THEREOF
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66.3%;
                                                                                                 11.9%;
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                                                                              Score 69.8; DB 6;
Pred. No. 5.3e-11;
0; Mismatches 42;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6e-12;
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FILE REFERENCE: CLOOISO6
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267
LENGTH: 4852
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                          SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 4855
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 266, Application US/60548091
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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Best Local Similarity 68.6%;
Matches 96; Conservative
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Best Local :
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Local Similarity 68.6%;
les 96; Conservative C
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  3632 GGCTGCCCTGCGCCACTACTACTTCACCAACAGCTGGAATATCTTCGACTTCGTGGTTGT 3691
                         135 CTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAAT 194
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Pred. No. 5.3e-11;
0; Mismatches 44;
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                                                                                                                                                        Score 69.6; DB 7;
Pred. No. 5.3e-11;
0; Mismatches 44
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Sequence 268, Application US/60548091

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 268
LENGTH: 4855
TYPE: DNA
ORGANISM: Homo sapiens
US-60-548-091-268
                                                                                                                                                                                                                                                                                                                                                                                          US-60-548-091-5582, Application US/60548091
; Sequence 5582, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
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US-60-548-091-268
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                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-548-091-5582
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5582
LENGTH: 201
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                                                                                                                                          Query Match 7.4%;
Best Local Similarity 72.7%;
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                                                                    CTTGGCCAAGATCAACCTGCTCTTTGTGGCCATCTTCACAGGCGAGTGTATTGTCAAGCT 3631
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    TCTTTCCATTGTTAGTA 274
                                           TGCCCTGCGCCACTACTACTTCACCAACAGCTGGAATATCTTCGACTTCGTGGTTGTCAT 62
                                                                                                                        Conservative
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Pred. No. 5.3e-11;
                                                                                                                   Score 43.4; DB 7;
Pred. No. 0.0012;
0; Mismatches 21;
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                                                                                                                        21;
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RESULT 8

Sequence 6751, Application US/10796280
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001510

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RESULT 9

US-10-796-280-6719

Sequence 6719, Application US/10796280

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001510

CURRENT APPLICATION UMBER: US/10/796,280

CURRENT FILING DATE: 2004-03-10
RESULT 10
US-10-796-280-6751
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; ORGANISM: Homo sapiens
US-10-796-280-6719
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; ORGANISM: Homo sapiens
US-60-548-091-5566
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CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5566
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LENGTH: 201
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001506
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                                                                                                                                                     103 ATGGTGCTCAAAATCATCGCCTTCAAGCCCAAGCATTACTTCACTGATGCCTGGAACACG 162
                                                                                                                                                                                            181 TGTCTCATCAAAATCTTTGCTTTGAGGC---AATACTACTTCACCAATGGCTGGAATTTA 237
                                                                                                                                                                                                                                                                 121 CCATGGAATCCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAA 180
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                                                                               TTTGACGCTCTTATTGTGGTGGGCAGCATAGTGGATA 199
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56.7%;
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Pred. No. 0.044;
1; Mismatches
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; Sequence 6815, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
; TITLE OF INVENTION: STENOSIS, METHODS OF DE
; FILE REFERENCE: CL001510
; CURRENT APPLICATION UNDER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
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Sequence 6783, Application US/10796280

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERAL OF DETECTION AND USES THEREOF
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; ORGANISM: Homo sapiens
US-10-796-280-6751
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US-10-796-280-6815
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CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6751
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/796,280 CURRENT FILING DATE: 2004-03-10 NUMBER OF SEQ ID NOS: 68533 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6783 LENGTH: 201
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Best Local Similarity
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Pred. No. 0.044;
1; Mismatches 64;
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Sequence 6873, Application US/10796280

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND FILE REFERENCE: CL001510

CURRENT APPLICATION NUMBER: US/10/796,280

CURRENT FILLING DATE: 2004-03-10

NUMBER OF SEQ ID NOS: 68533

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6873

LENGTH: 201
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: STENOSIS, METHODS OF DE
FILE REFERENCE: CLOO1510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 6853
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6845
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; ORGANISM: Homo
US-10-796-280-6815
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US-10-796-280-6873
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SEQ ID NO 6815
LENGTH: 201
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ORGANISM: Homo
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Pred. No. 0.044;
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RESULT 15
US-10-796-280-6903
; Sequence [6903; Application US/10796280
; Sequence [6903; Application US/10796280
; GENERAL INFORMATION: Michele et al.
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILLING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6903
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-6903
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Search completed: March 23, 2004, 04:50:45 Job time: 750.347 secs
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1 Similarity 56.7%; Pred. No. 0.044;
89; Conservative 1; Mismatches 64; Indels 3
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                 Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                  em_gss_mam:*
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                                                                                                                                                                                                                                                                                                              em_gss_vrt:*
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435
330
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29
            BX112455
AA885211
AA913881
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                                                                                                          SUMMARIES
BX112455 BX112455
AA885211 am34c11.s
AA913881 om21h12.s
AY404475 Homo sapi
                                                                  Description
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AQ743380 HS_5367_B	*	Ŋ	774	7.2	42.4	. <b>4.</b> 55	
34875 ENTCA8	AZ534	Ŋ	873	7.5		44	
42 F.	FRO	N	619		45.4	43	
6391	BX4	<u>_</u>	1126		46	42	
378	BXS	щ	658		48.6	41	
33126	BMe	н	502		50	40	
-	BW	щ	724	٠	50.2	39	
-	BW	Н	592		۲	38	
AZ081279 SCN4A Fel	AZ0	Ŋ	287	9.4	55	37	
_	CNS	Ŋ	840		5	36	a
Ψ,		_	561	٠	55.8	35	
	0 BF470392	ب	547	•	ıπ	34	
CD327202 AGENCOURT	_	ب	911		an a	ω G	
•		Н	674		~1	32	
AL706368 DKFZp686H		9	602	•	-1	31	
CD804204 UI-M-GV0-		Ļ	718	•	59	30	
CC586299 CH240_383		N	768	•		29	
538604 M		_	402	10.3	$\circ$	28	
CB520657 UI-M-GIO-		Ļ	768	٠	ω.	27	
Z86544 F.rubripes		Ŋ	604	•	64.8	26	a
maa38e08		Ļ	544		4.	25	
Pan t		Ŋ	5710	11.2	65.4	24	
AZ091181 RPCI-23-4		N	663	•	'n	23	a
100356	AU035605	9	778	11.5	67	22	
BX499931 DKFZp779F		щ	446		σ	21	
AL219260 Tetraodon		N	1043	•	9	20	
BQ731018 AGENCOURT		_	944		69.2	19	
<b>AMGNNUC</b>	4 CB613903	بر	553	•	69.8	18	
AA183990 ms53e02.r	AA183990	9	529		71	17	
AJ396135 AJ396135	AJ396135	Q	632	٠	71.8	16	
AL588672 AL588672	AL588672	9	610	٠	٠	15	
7 dac36	2 BG578677	ш	518			14	
199 Homo	9 AY416499	N	5943		•	13	
	AY41650	N	5666		٠	12	
220	1 AK083220	ш	4675			11	
Q946179 AGI	BQ94617	_	908	•	٠	10	
5148 UI-M-C	CF53514	بر	473		77.2	9	
Y267638 BY	BY26763	ш	402			8	
444 AMGN	CB6134	14	555	•	88.2	7	a
404477 Mus n	AY40447	N	4556	18.8	μ	6	
AY404476 Pan trogl	9 AY404476	N	3772	4.	143.6	տ	

EST 07-FEB-2003

ALIGNMENTS

RESULT 1 BX112455/c LOCUS

DEFINITION

BX112455 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE998BZ13715; IMAGE:1468724, mRNA sequence.

BX112455 Homo sapiens BX112455.1 sapiens (human) GI:27878914

1 (bases 1 to 523)
Ebert,L., Heil,O., Hennig,S., Neubert,P.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Partsch, E., Peters, M.

REFERENCE AUTHORS

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

COMMENT

TITLE

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH IM Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD IMAGD998B213715. RZPDLIB; I.M.A.GE. CDNA Clone Collection; Human UnigeneSet - RZPD3 (RZPDLIB NO.972) http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

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VERSION
                                                                                                                                                        RESULT 2
AA885211
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Matches 412;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        430 GGGAAGTTGCTAGGAGATAGGAGGCGGTAAATTTCTGGTTCCCCTTAACTCACTACACAA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 GÄAGTÄÄGTTTGTÄÄÄTCTTATCATTTTTTGAÄGTTTGTTCÄÄACTATCCACAÄÄGCÄGÄ
                                                                                                                                                                                                                                                                                                                   490 CTGAAATAGAGTTCAATAATCA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 TACCTARACCATGATTGGCTTGATGGCCTARATATACAACCAACCCCAAAGCCATGGAAT 129
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Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                              AA885211
A35 bp mRNA linear EST 04-JAN-1999 am34c11.s1 Soares NFL T GBC_S1 Homo sapiens cDNA clone IMAGE:1468724 3' SimiTar to TR:P70276 P70276 SODIUM CHANNEL, TYPE X, ALPHA POLYPEPTIDE ;, mRNA sequence.
AA885211
AA885211.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCGTGCTTCTTTCCATTGTTAGTAAGTAAATCAGCAGTCAGAGGGACTTTAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGTGCTTCTTTCCATTGTTAGTAAGTAAATCAGCAGTCAGAGGGACTTTAAGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT
                                                                                                                                                                                                                                                                                                                                                                       GGGAAGTTGCTAGGAGATA-----GAGAGTAATTTCTGTTCCCTTAACTCACTACACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-30287, 682632-687239, 726408-728711, and 72996-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/lab_host="DH10B"
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mol_type="mRNA"
  GI:2994288
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Pred. No. 1.4e-83;
0; Mismatches 22;
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RESULT 3 AA913881

LOCUS DEFINITION

AA913881 330 bp mRNA linear EST 10-JUN-1998 om21h12.s2 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 130 CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
                                                                                         316
                                                                                                                    310 GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGA 369
                                                                                                                                                                                  256
                                                                                                                                                                                                                                250
                                                                                                                                                                                                                                                                                                                       78 TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE Consortium (info@image.llnl.gov) for further possible reversed clone: similarity on wrong strand Insert Length: 561 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index 
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 435)
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                                                                                                                                                                                                                    GTCGTGCTTCTTTCCATTGTTAGTAAGTAAATCAGCAGTCAGAGGGACTTTAAGAACCA
                                                                                           GAAGTAAGTTTGTAAATCTTATCATTTTTTGAAGTTTGTTCAAACTATCCACAAAGCAGA
                                                                                                                                                                                                                                                                                 CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 195
                          AAACTGGGCCAAGTGTACTTTCTGAAAGAATAGACAGGGGTACTAATGCCATTCTCTACT
AAACTGGGCCAAGTGTACTTTCTGAGAGAATAGACAGGGGTACTAATGCCATTCTCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone libe Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco R1; a modified polylinker; Site 1: Not 1; Site 2: Eco R1; a modified polylinker; Site 1: Not 1; Site 2: Eco R1; a modified polylinker; Site 1: Not 1; Site 2: Eco R1; a modified polylinker; Site 1: Not 1; Site 2: Eco R1; and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-30287, 68263-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:1468724"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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96.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 316.8; DB 9
Pred. No. 4.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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REFERENCE
AUTHORS
TITLE
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AY404475
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                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE:1541735 3' similar to TR:P70276 P70276 SODIUM CHANNEL, TYPE X, ALPHA POLYPEPTIDE ;, mRNA sequence. AA913881 AA913881.1 GI:3053273 EST.
4614 bp DNA linear GSS 16-DEC-
Homo sapiens SCN11A gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 330)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                           GAAGTAAGTTTGTAA 324
                                                                                                                                                                                                                                                          GTCGTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGGGACTTTAAGAACCA 309
                                                                                                                                                                                                                                                                                                                                              TACCTAAACCATGATTGGCTTGATGGCCTAAATATACAACCCAACCCCAAAGCCATGGAAT 129
                                                                                                                                                      GAAGTAAGTTTGTAA 330
                                                                                                                                                                                                                                     GTCGTGCTTCTTTCCATTGTTAGTAAGTAAAATCAGCAGTCAGAGGGACTTTAAGAACCA
                                                                                                                                                                                                                                                                                                                 CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCCTAAACATGATTAGCATGATGGCTGAATCATACAACCAA-CCCAAAGCCATGAAAT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Soares_NFL T_GBC_S1"
/clone lib="Soares_NFL T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-30287, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 213.4; DB 9; Length 330; Pred. No. 4.7e-45;
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                                                                                                                                                                                                                                                                                                                                                                 250
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Inferring nonneutral evolution from human-chimp-mouse orthologous
1 (bases 1 to 3772)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
                                                                                                         Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                 Pan troglodytes SCN11A gene, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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AY404475.1
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                  GTCGTGCTTCTTTCCATTGTTA 271
                                                                                                                                                                                                                                                                                                                                                                                                     AAAATCTTTGCTTTGAGGCAATACTACTTCACCAATGGCTGGAATTTTATTTGACTGTGTG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATC 3690
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                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus_tag="HCM1903"
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                                                                                                                                                                 GI:39760453
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93.6%;
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                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                      DNA linea:
L TRANSCRIPT,
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                    Murphy, B.,
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AY404477
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark,A.G., Glanowski,S., Nielson,R., Iu,F., Murphy,B., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Iu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and orderin
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 4556)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera; S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Science 302 (5652), 1960-1963 (2003)
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                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY404477 4556 bp DNA linear GSS 16-DEC-
Mus musculus SCN11A gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence
AY404477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14671302
Submitted (16-NOV-2003) Celera Rockville, MD 20850, USA This sequence was made by seque them based on alignment.
                                                                                                                                                                                               Science 302 (5652), 1960-1963 (2003)
14671302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAATTTATTTGACTGTGTGGTCGTCTTCTTTCCATTGTTA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAACCCAAAGCCATGAAATCCATCCTTGACCATCT-CAACTGGGTCTTTGTGGTCATCT
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Location/Qualifiers
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/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="SCN11A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'locus_tag="HCM1903"
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Pred. No. 9.7e-27;
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                    sequencing genomic
                                                           Genomics, 45 West Gude Drive,
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                    exons and ordering
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CB613444/c
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Best Local Similarity
Matches 149; Conserv
                                                                              Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                           548 GAAGGAAACCTTCGATATCCTCAACATAGCATTCGTGGGCATCTTAACCATAAAGTGTCT
                                                    126 GAATCCATCCTTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCT
 555 bp
AMGNNUC:CDRG2-00013-C5-A cdrg2 (
cdrg2-00013-C5 5', mRNA sequence
CB613444
CB613444.1 GI:29573332
EST.
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Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                       Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                    Plate:
                                                                                                                                                                                                                                                                               One Amgen Center
Tel: 805 447-4881
                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCTTTCCATTGTTA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGACCATCTCCAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACATGATTATCATGATGGCTGAATCTGAAGGCCAGCCC--AACGAAGTGAAGAAAATC
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                                                                               Conservative
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                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="ttaxon:10116"
/clone="cdrg2-00013-c5"
/tissue_type="peptide and housekee"
/clone_Iib="cdrg2 (10902)"
/note="Vector: multiple; peptides and housekeeping"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                             Center Drive, Thousand Oaks,
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'locus_tag="HCM1903"
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/db_xref="taxon:10090"
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/mol type="genomic DNA"
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                                                                                           15.1%;
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Pred. No. 6e-18;
0; Mismatches
                                                                               Score 88.2; DB 10
Pred. No. 2.6e-12,
0; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nikaido, I., Satto, N., Satto, R., Satto, H., Nikaido, I., Osatto, N., Satto, R., Sattoki, H., Yamanaka, I., Niyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gorbani, L.E., Couslin, S., Dalla, E., Dragani, T.A., Chothia, C., Corbani, L.E., Couslin, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kanaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numatta, K., Okido, T., Pavan, W.J., Pertrea, G., Peoole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Vangier, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Winning, L. G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yangisawa, M., Yang, I., Mixi, T., Nakai, K., Kawai, J., Aizawa, K., Yangiswa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs 122656851

Bed 1246683
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                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Myazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sabakin,Sasaki,D., Sato,K., Shibata,K.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
General Research (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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Contact: Yoshihide Hayashizaki
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genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCTTTGCTTTGAGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 bp mRNA linear EST 12-SEP.
UI-M-GIO-chg-j-20-0-UI.r1 NIH BMAP_GIO Mus musculus cDNA clone
IMAGE:30536971 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)
                                                   Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGGAATGT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                      malia; Eutheria;
(bases 1 to 473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (house mouse)
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                   Location/Qualifiers
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/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 77.2; Db 1.,
Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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BQ946179
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VERSION
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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BQ946179.1
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                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CDNA Sequencing by: Agencourt Biosocience Corporation

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ946179 908 bp
AGENCOURT_8926526 NIH_MGC_94 Mus
5', mRNA sequence.
                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13998 row: c column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTAGTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTACTATTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATTCTCTCCATT
                                                                             quality sequence stop: 596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:30536971"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab host="DHIOB (T1 phage resistant)"
/clone_lib="NIH_BMAP_GIO"
/note="Organ: Brain, Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain, Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         program coordinator."
                                              Location/Qualifiers
organism="Mus musculus"/
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Pred. No. 1.9e-09;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA line
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e IMAGE:6469275
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Best Local &
                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                   Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
The RIKEN Genome Exploration Research Group Phase II Team and the
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/tissue_type="retina"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC 94"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size_3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
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/db_xref="taxon:10090"
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74.6%;
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Rodentia;
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Pred. No. 2e-09;
0; Mismatches 33;
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Sciurognathi; Muridae; Murinae; Mus
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Best Local (
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2438
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                                                                                                                                                                                                                                                          148 AACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCAACAAATCTTTGCTTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                   Similarity 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 420, 563-573 (2002) 6 (bases 1 to 4675)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                 GTGGGAATGT 2447
                                                    GTTAGTAAGT 277
                                                                                                              CACTACTATTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATTCTCCATT
                                                                                                                                                                                                                       AATCTGGTCTTCGTCATCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGA 2377
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative sodium channel, voltage-gated, type VIII, a sodium channel, voltage-gated, type VIII, a polypeptide (MGD|MGI:103169, GB|NM_011323, BLASTN, 99%, match=3589)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="hippocampus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain="C57BL/6J"
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lone="C630029C19"
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_xref="MGI:2417601"
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                                                                                                                                                                                                                                                                                                                                 Score 77.2; DB 11;
Pred. No. 2.2e-09;
D; Mismatches 33;
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                                                                                                                                    Homo sapiens SCN8A gene, genomic survey sequence. AY416499
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5943).

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 5666)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Toodd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rockville, MD 20850, USA
This sequence was made by sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-2003) Celera Genomics,
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                                                                                                                                                                                                                                                                                                                                                CACTACTATTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATTCTCTCCATT
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                                                                                     sapiens (human)
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/db_xref="taxon:10090"
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Eutheria; Rodentia;
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Pred. No. 2.3e-09;
0; Mismatches 33;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
1 (bases 1 to 518)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bo Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., Mc Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
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This sequence was made by sequencing genomic exons and order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Adams,M.D. and Cargill,M. Shinsky,D. and Cargill,M. 
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Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                   Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
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Library constructed by Life Technologies. DNA Sequencing Washington University Genome Sequencing Center
                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG578677.1 GI:13593741
                                                                      Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roslin Institute
Roslin, Midlothian, EH25
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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Contact: Frazer Murray
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                     Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IhAGE:4409085"
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/clo
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                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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Pred. No. 3.5e-08;
D; Mismatches 41;
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	Search completed: March 22, 2004, 23:13:23  Job time : 3445.35 secs	Search comp Job time :
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	267 TGTTAGTAAGT 277	Ş
TGATTCTGTCCAT 336	277 GCACTACTACCTTCACCATTGGGTGGAACATCTTTGACTTCGTTGTTGTTGTTCTGTCCAT	B S
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TGTTCGCCTTGCG 276	217 CAACCTGGTGTTCGTCATCTTCTTCACCTGCGAGTGTGTGCTGAAGATGTTCGCCTTTGCG	Db Ad
TCTTTGCTTTGAG 206	147 CAACTGGGTCTTTGTGGTCATCTTTACGTTAGAATGTCTCATCAAAATCTTTGCTTTGAG	92
610; 0; Gaps 0;	Query Match 12.3%; Score 71.8; DB 9; Length 610; Best Local Similarity 71.8%; Pred. No. 5e-08; Matches 94; Conservative 0; Mismatches 37; Indels	Query Match Best Local   Matches   9
daptor sequence: 5' purchased from	unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3'; 3' adaptor sequence: 5' GCGGCCGCTTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6854-1)"	ORIGIN

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Minimum
Maximum
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. Score 338.7 388.7 388.7 388.7 388.7 115.6 115.7 115.6 115.7 115.6 115.7 52 6528 5419 541 5860 6237 167476 Length DΒ 10 2 66222610 99991 10 10 10 AX017233 BD138455 AR340678 AF188679 AC116038 BD012082 BD082951 AF109737 HSA417790 RNO237852 AR340646 BD217791 AX017217 BD0138440 AC0127824 AC127824 AC127824 AC127824 AC127824 AC127824 AC127825 AF118044 AC126287 AL158215 AL1583718 AL1533718 AL1553718 AL155371 AX017233 Sequence BD138455 Mammalian AR340678 Sequence AF188679 Homo sapi BC12082 Human sod AF109737 Homo sapi BD012082 Human sod BD082951 Human sod AF109737 Homo sapi AJ417790 Homo sapi AJ417791 Regulatio AX017217 Sequence BD217791 Regulatio AX017217 Sequence BD118440 Mammalian AF659030 Rattus no B36122 Nucleic aci AC117294 Rattus no AC1277815 Rattus no AC1277815 Rattus no AC1277827 Regulatio AF118044 Mus muscu AB031389 Mus muscu AB031389 Mus muscu AB031389 Mus muscu AC126287 Rattus no AL158015 Homo sapi AL153778 Human DNA Continuation (10 o AL158015 Human DNA CONTINUATION OUS BUSCU AC1277282 Mouse DNA AC0135178 Mus muscu AC1277282 Rattus no AC127736 Rattus no AC127758 Rattus no AC127758 Rattus no AC127758 Rattus no AC127758 Rattus no AC13774 Mus muscu AC12758 Rattus no AC115748 Mus muscu AC11374 Mus muscu AC11374 Mus muscu AC115748 Rattus no AC109436 Rattus no AC105146 Rattus no AC105147332 Homo sapi Description

## ALIGNMENTS

from Patent W09947670.  GI:10042153  (human)  etazoa; Chordata; Craniata; Vertebrata; theria; Primates; Catarrhini; Hominidae; cose, D.T. and Hick, C.A. dium channel proteins dium channel proteins dium channel proteins	REFERENCE 1 AUTHORS Tate, S. TITLE Mammali JOURNAL Patent:	ORGANISM Homo sapiens Eukaryota; M Mammalia; Eu	ION ION	
	N., Grose,D.T. and Hick,C.A. an sodium channel proteins WO 9947670-A 17 23-SEP-1999;	plens piens La; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; a; Eutheria; Primates; Catarrhini; Hominidae; Homo.	17 irom Patent W0994/670. 3 3.1 GI:10042153	DNA

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the number of results predicted by chance to have a

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RESULT 2
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PF 18-MAR-1999 JP 2000536853

PR 18-MAR-1998 GB 9805793.8

PR 18-MAT T1998 GB 9805793.8

PI DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE C12N15/09, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, EC12N1/15,
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 223)
Grose, D.T., Hick, C.A. and Tate, S.N.
Mammalian sodium channel protein
Patent: JP 2002508941-A 16 26-MAR-2002;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 100.0%; ilarity 100.0%; Conservative 0,
                                                                                                                                                                                              Mammalian sodium channel protein 
Key Location/Qualifiers
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JP 2002508941-A/16
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                                                                                                                                              /organism='Homo sapiens (human)'
Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 5.4e-56;
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Sequence
AR340678
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                                                                                                        6237
Homo sapiens voltage-gated so
(SCN11A) mRNA, complete cds.
AF188679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 5860)
Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels
Patent: US 6573067-A 41 03-JUN-2003;
Location/Qualifiers
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                                                                      Homo sapiens (human)
                                                                                              AF188679.1 GI:6572949
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/mol_type="genomic
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             Cummins, T.R.,
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Submitted (21-8EP-1999) Neurology, Yale University/VAMC, 127A, Bldg.34, 950 Campbell Ave., West Haven, CT 06516, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ganglion neurons
FEBS Lett. 462 (
20047838
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                                                                                                                                              /rpt_family="Alu-Sc"
/rpt_type=dispersed
6165. .6170
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LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
RTLRALRPLRALSQFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
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WCRKQNLPQQKEVAGGCAAQSKOIIPUMEMKIGSETGELLGIITSVPKTLGVRHDWT
WLAFLAEEEDDVEFSGEDAQRITGFBFEQQAYELHQENKKFYSQRVQSVEIIMWFSB
EPHLTIQDFRKKSDVTSILSECSTIDLQDGFGWLPEMVPKKQPERCLPKGFGCCFPCC
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CLKIIALDPYHYFRRGNNIFDSIVALLSFADVKNCVLQKRSWPFLRSFRVLRVFKLAK
SWPTLNTLIKIIGNSVGALGSLTVLVIVIFIFSVVGMOLFGRSFNSQKSPKLCNPTG
PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENNWECMQEANASSSLCVIVFILITVIG
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SYFTPKKRKLFGNKKRKSFFLRESGKDQPPGSDSDEDCQKKPQLLEQTKRLSQNLSLD
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GSLNLKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLLSIVSTMISTLENQEHIPFPPTLFRIVRLARIGRILRLVRAARGIRTLLFALMMSL
PSLFNIGLLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSMLCLFQISTSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQXKLGG
QDIFMTEEQKKYYNAMKKLGSKKPQKFIPRPLNKCQGLVFDIVTSQIFDIIIISLIIL
NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGMNLFDCVV
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GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKRTIYR
                                                                                                                                                                                                                                                                                                                                                                                                                   TEESEDPLGEDDFDIFYEVWEKFDPEATQFIKYSALSDFADALPEPLRVAKPNKYQFL
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                /gene="SCN11A"
/note="polyA_signal"
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Length 6237;
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                                                                                                                                                                                                                                                                                                                    Submitted (07-OCT-2003) Genome Center, University of Washington, Box 352145, Seattle, MA 98195, USA On Oct 7, 2003 this sequence version replaced gi:21622736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome
AC116038
AC116038.3 GI:37537604
                                                                                                                                                                                                                                                                                                                                                                                                                                         Box 352145, Seattle, WA 98195, USA
(bases 1 to 167476)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 167476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaul,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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1,R.K., Olson,M.V., Raymond,C.
Sequencing vector; plasmid; 100% of reads chemistry: Dye-terminator ET; 45% of reads chemistry: Dye-terminator ET; 45% of reads chemistry: Dye-terminator Big Dye; 55% of reads Assembly program: Phrap; version 0.990319 consensus quality: 167467 bases at least Q40 consensus quality: 167476 bases at least Q20 consensus quality: 167476 bases at least Q20
                                                                                                                                                                      Center clone name: RP11-134J21 (bc0780)
                                                                                                                                                                                       Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                           Center: University of Washington Genome Center Center Code: UWGC
                                                                                                                                                                                                                                                          Web site: http://www.genome.washington.edu
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WA 98195, USA
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RP11-134J21, complete sequence.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Sequence Quality Assessment:
This entry has been annotated with sequence quality
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp. Base-by-base quality values are
not generally visible from the GenBank flat file formate
but are available as part of this entry's ASN.1 file. Overlapping Sequences: 5': RP11-1114A3 AC137625, 2001-bp overlap 3': RP11-182A24 (UWGC:bc0782) AC123903, 41341-bp overlap Sequence Validation: SeqDerMap This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. Insert size: 167476; sum-of-contigs Quality coverage: 18.9x in Q20 bases; sum-of-contigs EcoRI FngrPrnt <800 <800 <800 <800 SeqDerMap HindIII FngrPrnt <800 <800 SeqDerMap BglII FngrPrnt 1620 -----775 -----19834 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800 <800

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PN WO 0190355-A/1

PD 29-NOV-2001

PD 11-JUL-2000 WO 2000JP004629

PR 23-MAY-2000 JOOP 152085

PI ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
PC C12N15/12, C07K14/47, C07K16/18

CC

FH Key LOCALION/Qualifiers

FT CDS (200) . (5575).
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1 (bases 1 to 6528)
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WO 0190355-A/1.
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                                                                  ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCA 124
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FI CCC PF PR OS
                                         Homo sapiens
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  (bases 1 to 6528)
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5583 CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCCTCAGCCTCTGAGCTCCAGGGGTCA 5642
Homo sapiens voltage-gated sodium channel alpha subunit SCN12AN (SCN12A) mRNA, complete cds.
AF109737
AF109737.1 GI:6693696
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JP 2001327294-A/1
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OS Homo sapiens (human)
PN JP 2001327294-A/1
PD 27-NOV-2001
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Human sodium channel SCN12A
Patent: JP 2001327294-A 1 27-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAGGTGACCAAAATGACTT-GGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA
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                                                                                                                                                                                                                GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 5681
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                                                                                                                                                                                                                                                                                                                                   CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCAGTCTCAGGCCTCTGAGCCTCCAGGGGTCA
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ICHIRO KANAZAWA, JUN GOTO, YOSHIHIRO TEI
C12N15/09, C07K14/47, C07K16/18//C12P21/02, C12P21/08, C12N15/00
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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97.3%;
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Pred. No. 5.1e-49;
0; Mismatches 5
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Best Local Similarity
Matches 213; Conserv
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20090626
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Submitted (27-NOV-1998) Neurology, Graduat
Tokyo University, 7-3-1 Hongo, Bunkyo-ku,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jeong, S.Y., Goto, J., Hashida, H., Suzuki, T., Ogata, K., Masuda, N., Hirai, M., Isahara, K., Uchiyama, Y. and Kanazawa, I. Identification of a novel human voltage-gated sodium channel alpha subunit gene, SCN12A Biochem. Biophys. Res. Commun. 267 (1), 262-270 (2000)
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Jeong, S.Y., Suzuki, T., Hashida, H.,
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ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCA 124
                                                              CCAAGGTGACCAAAATGACTT-GGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA 5522
                                                                                                                      CAAGGTGGACCAAAATGACTTGGGAAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA 64
                                                                                                                                                                                        Conservative
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WLAPLABEEDDVEFSGEDNAQRITQPEBEQQAYELHQENKKPGVQSVEIDMFSED
EPHLTIQDPRKKSDVTSILSECSTIDLQDGFGWLPENVPKKQPERCLPKGFGCCFCC
SVDKRKPPWVIWMLRKTCYQIVKHSWFESFIIFVILLSSGALIFEDVHLENQPKIQE
LLNCTDIIFTHIFILENVLKWVAFGFGKYFTSAWCCLDFIIVTSVTTLINLMELKSF
RTLRALRAPRAKLSQFESKVVVNALIGAIPAILNVLLVCLIFMLVFCILGYEFSKSF
GKCINGTDSVINYTIITNKSQCESGNFSWINQKVNFDNVGNAYLALLQVATFKGWMDI
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HFDERGDFLQRQFALSAVSILTITMKEGEKELPGCENLASKLVNNCCCPQHLCV
KKVLRTVMTDDFTELAITICIIINTVFLAMEHRMEASFEKMLNIGNLVFSIFTJAK
CLKIIALDPYHYFRRGMNIFDSIVALLSFADVMNCVLQKRSMPFLRSFRVLRVFKLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLFNIGLLLFLIMFIYAILGMNWFSKVNPESGIDDIFNFKTFASSMLCLFQISTSAG
WDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNMYIAVILENFNTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGG
QDIFMTEEQKKYYNAMKKLGSKKPQKFIPRPLNKCQGLVFDIVTSQIFDIIISLIIL
NMISMMAESYNQPKAMKSILDHLNWVFVVIFTLECLIKIFALRQYYFTNGMNLFDCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWPTLNTLIKIIGNSVGALGNLTVVLVIVIFIFSVVGMQLFGRSFNSQKSPKLCNPTG
PTVSCLRHWHMGDFWHSFLVVFRILCGEWIENMWECMQEANASSSLCVIVFILITVIG
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PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTTGLYSVFFFIVVIFLGSFYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKRTIYR
FSAKHALFIFGPFNSIRSLAIRVSVHSLFSMFIIGTVIINCVFMATGPAKNSNSNNTD
                                                                                                                                                                                                                                                                                                                                                                                                                VMDLPMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANPLKKLYEPIVT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
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/db_xref="GI:6693697"
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97.3%;
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                                                                                                                                                                                                               Score 199; DB 9; Length 6528; Pred. No. 5.1e-49;
                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5583 CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCCTCAGCCTCTGAGCTCCAGGGGTCA 5642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submitted (25-0CT-2001) Blum R., Institut fuer Physiologie, Submitted (25-0CT-2001) Blum R., Biedersteiner Strasse 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               אביים שבייט מאות ביינים שמות ביינים שמות ביינים שמות האות פיינים שמות ביינים ביינים ביינים שמות ביינים ביי
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Direct Submission
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22272672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAV1.9 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ludwig-Maximillians-Universitaet, 608, 80802 Muenchen, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Na (V) 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ417790.1 GI:22796539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2384689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 5681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 5419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kafitz, K.W.
                                  NLTLAVVTMAYEEQNKNVAAEIEAKEKMFQEAQOLLKBEKEALVAMGIDRSSLTSLET
SYFTPKTKILFGNKKKKSFFLRESGKOQPFGSDSDEDCQKKPOLLEQTKRLSQNLSLD
HPDEHGDPLGRQRALSAVSILTITMKEQEKSGEPCLPGEBILASKYLVMCCPQMLCV
KKVLRTVMTGPFTELATTICIIINTVFLAMEHHKMEASFEKMLNIGNLVFTSIF1AEM
CLKIIALDPYHYFRRGWNIFDSIVALLSFADVMCVLQKRSWPFLRSRRVLRVFKLRV
                                                                                                                                                                                                                                        GEVPQPRPQLDLKASRKLPKLYGDIPRELIGKPLEDLDPFYRNHKTFMVLNRKRTIYR
FSAKHALFIRGPFNSIRSLAIRVSVHSLFSNEIIGTVIINCVEMATGEAKNSNNTD
IAECVETGIYIFEALIKILARGFILDEFSFLADPMNMLDSIVIGIAIVSYIPGITIKL
LPLRTERVFRALKAISVVSRLKVIVGALLRSVKKLNNVIILTFFCLSIFALVGQQLFM
GSLNILKCISRDCKNISNPEAYDHCFEKKENSPEFKMCGIWMGNSACSIQYECKHTKIN
PDYNYTNFDNFGWSFLAMFRLMTQDSWEKLYQQTLRTGLYSVFFFIVVIFLGSFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                excitation"
SWPTLNTLIKIIGNSVGALGSLTVVLVIVIFIFSVVGMQLFGRSFNSQKSPKLCNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GOA:Q8NDX3"
/db_xref="SFTREMBL:Q8NDX3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="voltage-gated
/protein_id="CAD10507.1"
/db_xref="GI:22796540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="TTX-insensitive"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="NAV1.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="NAV1.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cel1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="mediates neurotrophin-evoked neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (6908), 687-693 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             voltage-gated sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1_line="SH-SY5Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type="neuroblastoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Konnerth, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sodium channel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires the sodium channel
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Sg

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JOURNAL
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AUTHORS
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KEYWORDS
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RNO237852
                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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Matches
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                                                                                                                                                                                                                                                             Direct Submission
Submitted (28-APR-1999) Tate S.N., Molecular Pharmacology.
GlaxoWellcome Research and Development, Medecines Research
                                                                                                                                                                                                                                                                                                                                                                                                                            Two sodium channels contribute to the TTX-R sodium current in primary sensory neurons
Nat. Neurosci. 1 (8), 653-655 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tate, S., Benn, S., Hick, C., Trezise, I
Costigan, M., Plumpton, C., Grose, D.,
Dale, K., Bountra, C. and Woolf, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ237852.1 GI:4741728 alpha subunit; sns2 gene; voltage-gated sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAITUS norvegicus mRNA for voltage-gated sodium channel alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                   Tate, S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus.
                                                                                                                                                                                                                                                                                                                                                                                  10196578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCC 5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGGTGGACCAAAATGACTTGGGAAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA
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                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 5849)
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                                                                                                                                                                                                                                       Wood Road, Stevenage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTLRALRPIRALSOFEGMKVVVNALIGAIPAILNVLLVCLIFWLVFCILGVYFFSGKF
GKCINGTDSVINYTIINKSQCESGNFSWINGKVNEDWGNAYLALLQVAFFKGWMDI
IYAAVDSTEKEQQPEFESNSLGYIYFVVFIIFGSFTINHFIGVIIDNENQQXKLGG
QDIFWTEQKKYYNAMKKLGSKKEPQKPIPRELNKCQGLVFDIVTSQIFDIIIISLIIL
MISWAESYNQPKAKKSILDHLWWYFVVIFTLECLIKIFALRQYFTMGWNLFDCVV
VLLSIVSTMISTLENGEHIPFPFILFRIVRLARIGRILLVRAARGIITLLFALMMSL
PSLENIGLLLFLIMFIYAILGRMWFSKVNDESGIDDIFWFKTEASSMLCLEGISTSAG
MDSLLSPMLRSKESCNSSSENCHLPGIATSYFVSYIIISFLIVVNYJAVLZNIENFNTA
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EPHLTIQDPRKKSDVTSILSEGTIDLQDGFGWLEMVPKKQPERCLPKGFGCFPCC
SVDKXKPPWYLWMNLKHCYQIVKHSWEESFITFVILLSGALIFEDVHLENQPKIQE
LLNCTDIIFTHIFILEMVLKWVAFGFGKYFTSAWCCLDFIIVIVSVTTLINLMELKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEESEDPLGEDDFDIFYEVWEKFDPEATQFIKYSALSDFADALFEFLRVAKFNKYQFL
VMDLFMVSEDRLHCMDILFAFTARVLGGSDGLDSMKAMMEEKFMEANFLKKLYEFIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttkrkeeergaaiiQkafrkymmkvtkgdQgdQndlengphsplQtlcngdlssfgva
                                                                                                                                                                                     Location/Qualifiers
'gene="sns2"
                        /tissue_type="dorsal root ganglia"
|. .5849
                                                                     /organism="Rattus norvegicus"
|mol_type="mRNA"
|strain="Sprague-Dawley"
|db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 136.6; DB Pred. No. 3e-30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trezise,D., John,V., Mannion,R.J., Grose,D., Gladwell,Z., Kendall,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                         Hertfordshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                         SG1 2NY, UNITED
                                                                                                                                                                                                                                                                Research Centre
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**FOCUS** 

TITLE

8 망 Ś 밁 ORIGIN

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TIMTDEFTELAITICIIINTVELAVEHHNMDDNLKTIIKIGNWVFTGIFIAEMCLKII
ALDPYHYFRHGWVFDSIVALLSLADVLYNTLSDNRSSFLASIKVLKVFKLAKSWFTL
NTLIKIIGHSVGALGNLTVULTIVVEJFSVCAMERSFLASIKVLKVFKLAKSWFTL
NTLIKIIGHSVGALGNLTVULTIVVEJFSVCAMERSFLASIKVLKVFKLAKSWFTL
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ESFAGENKDSILFDAF PWKEYDTDMALYTGGAGAPLAFLAVEDDVEYCEGGALFT
TESFAGENKDSILFDAF PWKEYDTDMALYTGGAGAPLAFLAVEDDVEYCEGGALFT
GHSAGVQAGDLFPETKQLTSFDDQGVEMEVFSEEDLHLSIQSFRKKSDAVSMLSECS
TIDLNDIFRNLQKTVSFKKQDFRCFFKGLSCHFLCHTCHKKSDAVMVLWMNIRKTCYQI
VKHSWFESFIIFVILLSGALIFEDVNLFSKKGPKCKTCTNGTDNIFTSIFLLEMILKYV
AFGFRKTTSAACWLDFLIVVVSVLSLMNLFSKKFGRCINCTDNIFTSIFLEMILKYV
VALISAIPALNACHLDFLIVVSVLSLMNLFSKKFGRCINCTDNIFTSIFLTALSQFEGKKVVV
XLISAIPALANCHLDFLIVVSVLSLMNLFSKKFGRCINCTDNINYLDFTSVPNRS
                                                                                                                                                                                                                                                                                                                                                          QCNISNYSWKVPQVNFDNVGNAYLALLQVATYKGWLEIMNAAVDSREKDEQPDFEANL
YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLG
TKKPQKFIFRPLNKCQAFVFDLVTSQVFDVIILGLIVLMIIMAESADQPKDVKKTF
                                           SCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTÄTEESEDPLGEDDFEIFYEVW
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FTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRK
                                                                                                                                                                                             DILNIAFVVIFTIECLIKVFALROHYFTNGWNLFDCVVVVLSIISTLVSRLEDSDISF
PPTLFRVVRLARIGRILRLVRAARGIRTLLFALMMSLPSLFNIGLLLFLVMFIYAIFG
MSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNFMLEAKEHCNSSSQD
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KKRKFFGSKTRKSFFMRGSKTAQASASDSEDDASKNPQLLEQTKRLSQNLPVDLFDEH
VDPLHRQRALSAVSILTITMQEQEKFQEPCFPCGKNLASKYLVMDCSPQMLCIKKVLR
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RTFRVFRALKAISVISGLKVIVGALLRSVKKLVDVMVLTLFCLSIFALVGQQLFMGIL
NQKCIKHNCGPNPASNKDCFEKEKDSEDFIMCGTWLGSRPCPNGSTCDKTTLNPDNNY
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aabpqprpqldlkasrklpklygdippelvakplbdldpfykdhktfmvlnkkrtiyr
fsakralfilgpfnplrslmirisvhsvfsmfiictviincmfmansmerspdndipb
HMEKMVKLRLKDRSSSSHQVFCNGDLSSLDVAKVKVHND"
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/protein id="CAB41850.1"
/db_xref="GI:4741729"
/db_xref="GOA:088457"
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/codon_start=1
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AR340646
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1 (bases 1 to 5875)
Dib-Hajj,S. and Waxman,S.G.
Nucleic acid encoding sodium channels in dorsal root ganglia
Patent: US 6573067-A 1 03-UUN-2003;
Location/Qualifiers
                                                                                   Unknown
                                                                                                                                          Sequence 1
AR340646
                                                                      Unclassified.
                                                                                                  Unknown.
                                                                                                                              AR340646.1
                                                                                                                                                                        AR340646
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                                                                                                                                                                                                                                                                                                                                                                                        CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                                                                                                                                                                                                                                    GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                                                                                                                                                                                                                                                                  GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                        TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                        from patent US 6573067.
                                                                                                                                GI:33732378
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Best Local Similarity
Matches 127; Conserv
                                                                                                                            Query Match
Best Local Similarity
Matches 127; Conser
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                                                                                                                                                                                                                                                                                              YALE UNIVERSITY
OS Rattus norvegicus (rat)
PN JP 2002509860-A/1
PD 02-ARP-2002
PF 29-JAN-1998 US 60/109402 PI
SULAYMAN DIB HAJJ,STEPHEN WAXWAN
PC CO7K14/435,A61K38/00,A61K39/395,A61K45/00,A61P25/04,A61P43/00,
PC C12N5/10,C12N15/09,C12P21/02,G01N33/566,G01N33/84,A61K37/02,
PC C12N5/00,
PC C12N5/00,
PC C12N5/00,
PC C12N5/00
CC cDNA sequence for rat NaN
CC n = a or c or g or t
FRey Location/Qualifiers
FT CDS (41). (5335)
FT unsure (4042).

Location/Califiers
(4042).
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                                                      5236 CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTTGCAATGGAGACTT 5295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 5875)
Hajj, S.D. and Waxman, S.
Regulation of sodium channel in posterior
Patent: JP 2002509860-A 1 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD217791 5875
Regulation of sodium channel
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GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGAGCCCTCACCTCCACGCC 134
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                                                                                       CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
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/mol_type="genomic DNA"
                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                       location/Qualifiers
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Pred. No. 2e-19;
0; Mismatches 44;
                                                                                                                          Score 100.6; DB 6;
Pred. No. 2e-19;
0; Mismatches 44;
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Murinae;
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1 from AX017217
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                                                                                                                                                    /translation="MEERY YED! FPDERNFR PFTSDS1AAIKKRIAIOKERKKSKDKA
AAEPQPR POLDLKASRKL PKLYGDL PELVTKP LEDLDPYYKOHKTEWVLNKKRTIYR
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YVF1G1Y ILLAVIK LLARGET VDERS FLADWNWLDF IV IGTAIATCF PGSQVLSAL
RTFR VFRALKAIS VISGLKVI VGALLRS VKKLVDVMVLTLFCLS I FALVGQQLFMGII
NQKCIKHNCGPNEASNKDCFEKEKDSEDF INCGTWLGSR PCPRGSTCDKTTLNPDNNY
TKFDNGWSFLAMFR WMTQDSWERLLRSGILKTYGIV FVFFFVVVI FLGSFYLLNTLA
VVTMAYEBQNRNVAAETEAKERMFQEAQQLLREEKEALVAMGIDRSSLOSLQASSFS
KKRKFFGSKTRKS FFNRGSKTAQASASDEDDAS KNPQLLENGSTCDKTTLNPDNNY
TKFDNGWSFLAMFR WMTQDSWERLLRSGIV TVVFFFVVVI FLGSFYLLNTLA
VVTMAYEBQNRNVAAETEAKERMFQEAQQLLREEKEALVAMGIDRSSLOSLQASSFS
KKRKFFGSKTRKS FFNRGSKTAQASASADSEDDAS KNPQLLENGTRLSGYNLLVTLA
VTMAYEBQNRNVADSI VALLSLADVLYNTLSDNNRSFLASIR VLAVFKLAKGMFTL
NTLIKI IGHSVGALGNITVUTI I VTVFLAVEHHNMDDNLKTILKIGNWVFTGIF I AEMCLKI I
ALDPYHYFRHIGWNVEDSI VALLSLADVLYNTLSDNNRSFLASIR VLAVFKLAKGMFTL
NTLIKI I GHSVGALGNITVUTI I VTVFLYNTLSDNNRSFLASIR VLAVFKLAKGMFTL
NFYHSETUVFRILCCEMI ENNWGCMQDMDGSPLCI I VFVLIMVIGKLVULLF I ALLL
NSFSNEEKDGSLEGETRKTKVQLALDRFRARSFMLHALQSFCCKKCRKNSPKRET
TESPAGENKOSILPDARFWKSYDTDWALYTGQAAPLAFLAEVEDDVEYCGEGGALFT
SQHSAKVQAGDLPFETKQLISEDDQGVEMEVESEBDLHLSIQSFCKKCERKNSPKRET
TESPAGENKOSILPDLYSUFSDDQGVEMEVESEBDLHLSIQSFCKKCERKNSPKNET
SQHSAKVQAGDLPFETKQLISEDDQGVEMEVESEBDLHLSIQSFCKKTYNAMKKLG
VKHSWESKYDVALVELIGUTSOFTEVNILPSLROUTSKEEDSDFEANL
YALLSVUFFTISAKCHVSVLSIANNLFSEROUTSKEEDSDFEANL
YALLSVUFFTISAKCHVSVLSIANNLFSEROUTSKEEDSDFEANL
YALLSVUFFTISCLIKVFALRQHYFTNGMNLFSCKFGREINGTDINMYLDFTEVBREEDSDISF
DILNIAFVUFFTSAKCHVSVLTAARGINTLLFALMMSLDSLFNIGGLLEDSDISF
DILNIAFVUFFTSCHLCUXDAARGINTLLFALMMSLDSLFNIGGLLLEDNDISF
DFTLFRVVKLGRGINDI FWFFTSCHMICTSCHTTAAMMSLDSLFNIGGLLLEDNDISF
DFTLFRVKRAGRINGTSTALLVRAARGINTLLFALMMSLDSLFNIGGLLLEDNDISF
DFTLFRVKRAGSTOD
MSMEKKYKNGGSOD
                                                        MSWFSKVKKGSGIDDIFNFETFTGSMLCLFQITTSAGWDTLLNPMLEAKEHCNSSSQD
SCQQPQIAVVYFVSYIIISFLIVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVW
EKFDPEASQFIQYSALSDFADALPEPLRVAKENKFQFLVMDLEMVMGDRLHCMDVLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
MEKMVKLRLKDRSSSSHQVFCNGDLSSLDVAKVKVHND"
                                   FTTRVLGDSSGLDTMKTMMEEKFMEANPFKKLYEPIVTTTKRKEEEQGAAVIQRAYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAC07697.1"
/db_xref="GI:10042138"
/db_xref="REMTREMBL:CAC07697"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="unnamed protein product"
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Patent WO9947670.
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Query Match Best Local S Matches 127

al Similarity 74.

74.3%;

Score 100.6; DB 6; Pred. No. 2e-19; 0; Mismatches 44;

Length 5897;

0,

Gaps

0

0;

Murinae;

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REFERENCE
AUTHORS
TITLE
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BD138440
                                                  RESULT 15
AF059030
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KEYWORDS
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     DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: JP 2002508941-A 1 26-MAR-2002;
GLAXO GROUP LTD
OS RATURE NOTVEGICUS (rat)
PN JP 2002508941-A/1
PD 26-MAR-1909
PD 19-MAR-1999 JP 2000536853
PR 18-MAR-1998 GB 9805793, 8
PR 18-MAR-1998 GB 9805793, 8
PR DAVID THOMAS GROSE, CAROLINE ANNE HICK, SIMON NICHOLAS TATE PC C12N15/9, A61K45/00, A61P17/04, A61P25/02, C07K14/705, C07K16/28, PC C12N15/5,
AP059030 Sport AP059030 RNA linear ROD 16-JUL-2001 RATTUB NOT VERY RATTUB NOT VERY ROLL NAN MRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      LS CAAAATGACTTGGGAAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC
C12N1/19,C12N1/21,C12N5/10,C12Q1/02,G01N33/15,G01N33/50,G01N33/ PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grose, D.T., Hick, C.A. and Tate, S.N. Mammalian sodium channel protein Patent: JP 2002508941-A 1 26-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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JP 2002508941-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BD138440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT 5303
                                                                                                                                                                                                                    TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGGTCAG 185
                                                                                                                                                                                                                                                                                                                 GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                   CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTTGCAATGGAGACTT 5303
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                                                                                                                                                                    TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG 5414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian sodium channel protein
Key Location/Qualifiers
CDS (49). (5346).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C12N15/00, C12N5/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%;
74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100.6; DB 6;
Pred. No. 2e-19;
0; Mismatches 44;
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l protein.
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AUTHORS
TITLE
JOURNAL
                                                     polyA_signal
ORIGIN
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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MEDLINE
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-APR-1998) Neurology, Yale University Medica 333 Cedar St, New Haven, CT 06510, USA On Jul 16, 2001 this sequence version replaced gi:3372614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dib-Hajj,S.D., Tyrrell,L., Black,J.A. and Waxman,S.G. NaN, a novel voltage-gated Na channel, is expressed preferentially in peripheral sensory neurons and down-regulated after axotomy proc. Natl. Acad. Sci. U.S.A. 95 (15), 8963-8968 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dib-Hajj,S.D., Tyn
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
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AF059030
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKFDNFGWSFLAMFRVMTQDSWERLYRQILRTSGIYFVFFFVVVIFLGSFYLLNLTLA
VQTMAYSEQNRNVAASTBAKERNFQBAQQLLREKERALVAMGIDRSGLWSLQAASFSB
KKRKFFGSKTREKSFYRAGSADSEDDASKNPQLLEDGTKRLSQNLVSLQAASFSB
KKRKFFGSKTREKSFYRAGSADSEDDASKNPQLLEDGTKRLSQNLVDLDEDEL
VDPLHRQRALSAVSILTITMQEQEKFQEPCFPCGKNLASKYLVMDCSPQMLCIKKVLR
TIMTDEFTELAITICIIINTWFLAVEHINMDDNLKTILKIGMSVMTFTGLFIASMCIKI
ALDPYHYFRHGMNVFDSIVALLSLADVLYNTISDNNRSFLASLRVLRVFKLAKSMFTL
NTLIKIIGHSVGALGNLTVVLTIVFFIFSVCGNRLFGTKFNKTAYATQERPRRWHMD
NFYHSFLVVFRILCGEMIENMGCMQDMDGSPLGIIVFVLINGKLVTANLFJALLL
NSFSNEEXDGSLEGETRKTKVQLALDRFRRAFSFMLHALSFCCKKCRRKNSFXFKF
TESFAGENKDSILPDAFFKKEYDTDMALYTGQAGAPLAFLAFWEDDVEKGGGGALFT
TESFAGENKDSILPDAFFKKEYDTDMALYTGQAGAPLAFLAFVEDDVEKGGGGALFT
TGSFAGENKDSILPDAFFKKEYDTDMALYTGQAGAPLAFLAFVEDDVEKGGGGALFT
TGSFAGENKDSILPDAFFKKEYDTDMALYTGQAGAPLAFLAFVEDDVEKGGGGALFT
TGSFAGENKDSILPDAFFKKEYDTDMALYTGQAGAPLAFLAFVEDDVEKGGGGALFT
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TGSFAGENKDSILPDAFFKKGLTSPDDQAVEMEVETSEEDLHLSIGSFKKGDAVGNLSECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="meeryypvifpdernfrpftsdslaaiekriaiqkerkkskdka aabeqpreqldlkasrklykdiperlvakpledldpfykdhkktryvlnkkrtiyr rabeqpreqldlkasrklpklygdippelvakpledldpfykdhkktryvlnkkrtiyr fsakkalpilgernflarifispelyvlfictiincmfmansmersfdndipe yvfigiyileaviktlargffvdefsflrdmwidbfivigfaiatcepsgovnlsal rtfrveralkaisvisglkvuvgallrsvkklydvmvltlfclsifalvgoqlfmgil nqkcikhncgpppasnkdcfekekdsedfikgcgtwlgsrpcpngstcdkttlnddnvr
                                                                                                                                          HMEKMVKLRLKDRSSSSHQVFCNGDLSSLDVAKVKVHND'
                                                                                                                                                                                          SCQQPQIAVVYFVSYIIISFLIVVNMYIAVILENFNTATEESEDPLGEDDFEIFYEVW
EKFDPEASQFIQYSALSDFADALPEPLRVAKENKFQFLVMDLEMVMGDRLHCMDYLFA
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YAYLYFVVFIIFGSFFTLNLFIGVIIDNFNQQQKKLGGQDIFMTEEQKKYYNAMKKLG
TKKPQKFIFRFLNKCQAFVFDLVTSQVFDVIILGLIVLMIIMAESADQPKDVKKTF
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VKHSWFESFIIFVILLSSGALIFEDVNLPSRQVEKLERCTDNIFTFIFLEMILKWV
AFGFRRYFTSAMCYLLDFLIVVVSVLSLMNLPSKJSFRTLRALRPLRALSQFEGMKVVV
YALISAIPAILNVLLVCLIFWLVFCILGVNLFSGKFGRCINGTDINMYLDFTEVPNRS
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="voltage-gated Na channel alpha subunit NaN"
/protein_id="AAC40199.1"
/db_xref="GI:3372615"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="TTX-R voltage-gated Na channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="dorsal root ganglia"
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     Score 100.6;
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Result
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Listing
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Copyright (c) 1993 - 2004
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geneseqn2001bs:*
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                   AAK42749
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AAF30102
AAF30102
AAF21480
ADB52919
ADD321911
AAK60241
AAX60241
AAX60241
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Aax87600 Rat sodiu
Aaf30102 Rat senso
Adb52929 Primary r
Add32191 Rat Na v
Aax60241 CDNA enco
Aax87601 Mouse sod
Aaf30103 Mouse sod
Add32195 Mouse Na
Aax60244 Stabilise
Adx3209 Rat Na v
Aax670962 Human imm
Aak70963 Human imm
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Add32193
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29.8	29.8	29.8	30	30	30	30	30	30.2	30.4	30.4	30.4	30.4	30.6	30.6	30.6	30.6	30.6	31.4	31.4	31.4	31.4
13.4	13.4	13.4	13.5	13.5	13.5	13.5	13.5	13.5	13.6	13.6	13.6	13.6	13.7	13.7	13.7	13.7	13.7	14.1	14.1	14.1	14.1
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ABL22855	ACF66511	ADE76297	AAH26495	AAD48135	AAF21860	AAH26494	AAV32838	AAX86269	ABL68122	ABV75557	AAH14551	ADB50969	ACA63042	ACA63043	AAL54471	AAL54470	ABK49423	ABV35555	ABV44363	ABV05305	ABV14474
Abl22855 Drosophil	Acf66511 Photorhab	Ade76297 Human BSK	Aah26495 Human low	Aad48135 Human VIP	Aaf21860 Human bre	Aah26494 Human low	Aav32838 Human low	Aax86269 DNA encod	Abl68122 Ovary can	Abv75557 Saccharop	Aah14551 Human cDN	Adb50969 Primary r	Aca63042 Human Cad	Aca63043 Human Cad	Aal54471 Human cad	Aal54470 Human cad	Abk49423 DNA encod	Abv35555 Human pro	Abv44363 Human pro	Abv05305 Human pro	Abv14474 Human pro

## ALIGNMENTS

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RRSULT 1
AAZ2145
IID AAZ22
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AAZ2145
AC AAZ2
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BOT 03-D
DT 03-
Query Match
Best Local Similarity
Matches 223; Conserv
                                                                                                                                                       Sequence 223 BP; 53 A; 64 C; 55 G; 51 T; 0 U; 0 Other;
                                                                                                                                                                                                                             AAZ21481 to AAZ21495 represent fragments of the human sensory neurone specific 2a (SNS-2a) is a sodium channel protein. SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators can be used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain; voltage gated; hypersensitivity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human sensory neurone specific 2a nucleotide sequence fragment #15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian sodium channel protein for treating pain and hypersensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grose DT, Hick CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 68; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1999;
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Pred. No. 2.6e-63;
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The present sequence is that of cDNA encoding a novel human tetrodotoxin CC resistant sodium channel, termed NaN (see AMB20121). The cDNA was CC isolated from a human dorsal root ganglia tissue cDNA library by PCR CC amplification (see also AMF30122-23). NaN belongs to the a-subunit CC voltage-gated sodium channel protein family and produces a TTX-R sodium CC current. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres. CC Preferential expression of NaN on sensory neurons innervating the body CC (dorsal root ganglia) and the face (trigeminal ganglia), but not on other CC neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed CC uses in relation to acute and/or chronic pain pathologies. A claimed CC in a human or animal subject involves administering an agent that alters sodium current flow through NaN channels, or which modulates cost transcription or translation of NaN mRNA, in dorsal root ganglia or trigeminal neurons. NaN nucleic acids are used in gene therapy to correct
                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1999;
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                                                                                                                                                                               Expression vector useful for stable cloning and expression of Navl.9 sodium channel at the mRNA and protein levels comprises a nucleic acid sequence that encodes a mammalian Navl.9 sodium channel protein or its
                                                                                                                                                                                                                                                                                                                                                  Gonda
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The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 19 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected

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Sodium channel-dependent sodium current by: (a) providing a cell that has the produce a cell that has cell channel-dependent sodium current by: (a) providing a cell that has cell channel conditions that allow expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein to produce a sodium current into the transfected cell; (a) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mann and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a human Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.
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Best Local S
Matches 214
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                                                                                               23-MAY-2000; 2000JP-00152085.
                                                                                                                                                            11-JUL-2000; 2000WO-JP004629
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                                     (NISC+) JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n; gene; ss; sodium channel subunit; SCN12A; SCN12A-s; SCN8A; n nervous system; chromosome 3p23-21.3; excitatory cell; development; familial hyperglycaemia; QT extending syndrome type r endplate disease.
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200. .5575
                                                                                                                                                                                                                                                                                                                                                              /product= "Human sodium channel subunit SCN12A"
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97.7%;
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Matches 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequence of three sodium channel subunits from the human nervous system (SCN12A, SCN12A-s and SCN8A). The SCN12A/SCN12A-s gene is found on chromosome 3p23-21.3 and the SCN8A gene is found on chromosome 12q13.1. The sodium ion channel subunit proteins are useful in studying physiological mechanisms relating to excitatory cells and in drug development. The sodium ion channel subunit proteins are useful for treating diseases such as familial hyperglycaemia, QT extending syndrome type 3 and motor endplate diseases. The present cDNA sequence encodes the human SCN12A sodium channel subunit
                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat sodium channel NaN cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channel; ion transport; rat; dorsal root ganglia; pain; a; hyperexcitability; therapy; Scnlla gene; 88.
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Pred. No. 7e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5875 BP; 1432 A; 1458 C; 1422 G; 1511 T; 0 U; 52 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1A-D; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-479168/40.
                                                                                                                                                                                                       Rat sodium channel NaN cDNA.
                                                                                                                                                                                                                                                      30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                       AAF30102 standard; cDNA; 5875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve cells in the brain and spinal cord. The NaN gene has been named
                                                                            Rattus norvegicus.
                                                                                                                        hyperexcitability; analgesic;
                                                                                                                                                  Sodium channel; NaN; rat; tetrodotoxin resistant; pain; paraesthesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY06596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGAGCCGTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGGTCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waxman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0072990P.
98US-0109402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US002008
  Location/Qualifiers 41. .5338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100.6; DB 2
Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                          B₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                           gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 7
AAZ21480
ID AAZ2
XX
AC AAZ2
XX
AC O3-L
XX

AAZ21480 standard; cDNA;

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03-DEC-1999 AAZ21480;

(first entry)

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                                                                                                                                                                                                                                                                                                                                             The present sequence is that of cDNA encoding a novel rat tetrodotoxin CC resistant sodium channel, termed NaN (see AAB20122). The cDNA was CC isolated from a dorsal root ganglia tissue cDNA library by PCR camplification using generic primers (from conserved resions of a-subunit sodium channel proteins) and NaN-specific primers (see also AAF30105-19), CC and RACE amplification. The open reading frame shows 73% similarity to CC the human NaN sequence (see AAF30101). NaN belongs to the a-subunit CC voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels underlie the generation and propagation of CC impulses in excitable cells such as neurons and muscle fibres. CC Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other current, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed current flow through NaN channels, or which modulates sodium current flow through NaN channels, or which modulates codison current flow through NaN channels, or which modulates codison current flow through NaN channels, or which modulates codisoners associated with decreased sodium channel expression or consistency to down-regulate NaN expression, in the diagnosis of disease, and in the recombinant production of NaN polypeptides
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paraesthesia and/or hyperexcitability phenomena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dib-Hajj S, Waxman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999;
                                                                                                                                                                                                                                                                                                                 Sequence 5875 BP; 1455 A; 1466 C; 1434 G; 1518 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB20122, AAB20123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-103147/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUL-2000; 2000WO-US019342
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5356
                                                                                                                                                           5236 CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT
                                      135
                                                                                                                                                                                                                                         127;
                                                                                                                  75
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                                                                                                                                                                                                                                                         Similarity
TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGCAGCGGCAG
                                    TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
                                                                             GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                                  GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC
                                                                                                                                                                                                CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                       45.1%;
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                                                                                                                                                                                                                                   Score 100.6; DB 4;
Pred. No. 1.8e-22;
0; Mismatches 44;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                   0 U; 2 Other;
                                                                                                                                                                                                                                                                          Length 5875;
                                                                                                                                                                                                                                     0;
  5406
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           5295
                                                                             5355
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RESULT 8
ADB52920
ID ADB5
XX ADB5
XX ADB5
XX ADB5
XX Prim
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KW toxi
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Best Local S
Matches 127
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                                                                                     toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes rat sensory neurone specific 2a (SNS-2a). SNS-2a is a sodium channel protein. SNS-2a can be used in a method for the identification of a modulator of a sodium channel, and for assaying for compounds which modulate sodium flux. The sodium channel modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
WO2003065993-A2
                                                                                                                                                                                  Primary
                                                                                                                                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                  ADB52929;
                                                                                                                                                                                                                                                                                                                                ADB52929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian sodium channel protein for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Page 52-58; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in a medicament for the treatment of pain or hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127;
                                            norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽.
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                                                                                                                                                                                rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY41668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG 5414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5897 BP; 1474 A; 1471 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e specific 2a; SNS-2a; sodium channel protein; pain;
hypersensitivity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-00005793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "sensory neurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                              DNA; 5905
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                                                                                                                                                                                                                                   entry)
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74.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100.6;
Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1435 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                      diagnostic marker;
                                                                                                                                                                                     SEQ ID NO:3471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypersensitivity
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                                                                                                                                                                            Query Match
Best Local Sim
Matches 127;
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09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                               compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene expression of a tissue or cell sample to a database of Tox mean and non-Toxic compounds.
                                                                                                                                                                                                                                    Sequence 5905 BP; 1476 A; 1471 C; 1439 G; 1519 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-731472/69.
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13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 44; SEQ ID NO 3471; 874pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-2002;
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19-APR-2002;
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                                                                                                                                                                                                                                                                    toxicity modelling related gene sequence from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for determining whether a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2003;
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                                                          5307
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                                                                                                                                                                                             Similarity
                                                                                                                                      CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
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TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG
                             TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG
                                                           GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                       GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC
                                                                                                                    CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0378665P.
2002US-0394230P.
2002US-0394253P.
2002US-0407688P.
2002US-0442900P.
                                                                                                                                                                              Conservative
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2002US-0378652P.
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2002US-0374139P.
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2002US-0373601P.
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2002US-0371135P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002US
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74.3%;
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                                                                                                                                                                                            Score 100.6; DB 9
Pred. No. 1.8e-22;
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                          DB 9;
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                                                                                                                                                                               Indels
                                                                                                                                                                                                       Length 5905;
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                                                                                  Matches
                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acsequence that encodes a mammalian Nav1.9 sodium channel protein or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003080570-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression vector; Na v 1.9 sodium channel protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat Na v 1.9 sodium channel protein encoding cDNA SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD32191 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonda MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2002; 2002US-0365550P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2003; 2003WO-US008611
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                                                                                                                                                              Sequence 5905 BP; 1476 A; 1471 C; 1439 G;
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DB; ADD32192.
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                                                                                                     Similarity
                                        CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Greenwood JD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1; 125pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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74.3%;
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                                                                              Score 100.6; DB 9
Pred. No. 1.8e-22;
D; Mismatches 44
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                                                                                                                                                              1519 T; 0 U; 0
                                                                                                                   DB 9;
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                                                                                                                                                                Other;
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ID AAX60
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNS. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating epilepsy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type 5 sodium channel; PN5; nervous system; plexiform; dorsal root ganglia; tetrodotoxin; TTX; epilepsy; stroke; diabetic neuropathy; traumatic injury; AIDS-related neuropathy; neuropathic pain; migraine; headache; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1A-E; 90pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietrich PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5908 BP; 1458 A; 1474 C; 1451 G; 1525 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a type 5 sodium PN5. The protein is a sodium ion channel of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated DNA encoding sodium channel of the nervous system
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                                                                                                                                                                                                                                             5274 CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT
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DB; AAY16572.
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                                                                                                                                                                                                                                                                                                CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT
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   TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG
                                                  TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG
                                                                                                                                                                       GTCTAGCTTTGGGGTGGGCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC
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                                                                                                                        GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
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74.38;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 100.6; DB : Pred. No. 1.8e-22;
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                                                                                                                                                                                This is the nucleotide sequence of an isolated nucleic acid which encodes the mouse NaN channel (see AAY06597), a previously unidentified voltage gated sodium channel protein that is preferentially expressed in dorsal root ganglia (DRG) or trigeminal ganglia, and which produces a TTX-R sodium current. The NaN channel cDNA was obtained from mouse trigeminal ganglia cDNA by PCR amplification using rat NaN-based primers (see AAX87660-19). Rat, mouse and human NaN nucleic acids (see AAX87600-02) and polypeptides (see AAY06596-98) are provided. The invention also includes expression vectors and transformed host cells, methods for identifying tissues and cells that express NaN, methods for identifying tissues and cells that express NaN, methods for identifying agents that modulate NaN channel activity or NaN channel mRNA transcription or translation, and a method for using such agents to treat acute or chronic pain, paraesthesia and hyperexcitability phenomena. The preferential expression of NaN in sensory DRG and trigeminal neurons provides a target for selectively modifying the behaviour of these nerve cells while not affecting other nerve cells in the brain and spinal cord.
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Best Local S
Matches 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dib-Hajj S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1998;
20-NOV-1998;
                                                                                                              Sequence 5822 BP; 1483 A; 1411 C; 1352 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYYA
                                                                                                                                                                  gene encoding NaN has been named Scnlla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sodium channel; ion transport; mouse; dorsal root ganglia; pain; ssthesia; hyperexcitability; therapy; Scnlla gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 7A1-3; 91pp; English
  Conservative
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5789. 5794
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98US-0109402P.
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The present sequence is that of cDNA encoding a novel mouse tetrodotoxin cresistant sodium channel, termed NaN (see AAB20124). The cDNA was CC isolated from trigeminal ganglia cDNA using primers (see AAF30120-21) cased on rat NaN sequences. Mouse NaN shows 68% similarity to human NaN (see AAB20121). The gene encoding NaN, termed Scnlla, is located on mouse chromosome 9. NaN belongs to the a-subunit voltage-gated sodium channel protein family and produces a TTX-R sodium current. Such channels cunderlie the generation and propagation of impulses in excitable cells such as neurons and muscle fibres. Preferential expression of NaN on sensory neurons innervating the body (dorsal root ganglia) and the face (trigeminal ganglia), but not on other neurons, makes it a very useful target for diagnostic and/or therapeutic uses in relation to acute and/or chronic pain pathologies. A claimed method of treating pain, paraesthesia and/or hyperexcitability phenomena in a human or animal subject involves administering an agent that alters sodium current flow through NaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding human tetrodotoxin resistant sodium channels, useful for preventing, diagnosing and treating pain, paraesthesia and/or hyperexcitability phenomena.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig 7A; 162pp; English.
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The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammallan Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron; mouse; gene;
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                                                                                                                                                                                                                                                                    Expression vector useful for stable cloning and expression of Nav1.9 sodium channel at the mRNA and protein levels comprises a nucleic acsequence that encodes a mammalian Nav1.9 sodium channel protein or it
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Na v 1.9 sodium channel protein encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gonda MA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003080570-A2
                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-876895/81.
P-PSDB; ADD32196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TRAN-) TRANSMOLECULAR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2002; 2002US-0365550P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGACTTGTCTAGCTTGGATGTGCCCAAGATCAAGGTTCATTGTGACTGAAACCCCCCAC 5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÁAGATGÁTCÁAGCTGÁAGCTGAÁAGGCAGGTCAAGTTCÁTCGCTCCAGGTGTTTTGCAAT 5265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenwood
                                                                                                                                                                                  SEQ ID NO 5; 125pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product= "Na v 1.9 sodium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.7%;
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Pred. No. 8.4e-18;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1362
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                                                                                                                                                                                                                                                                 a nucleic acid
protein or its
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a mouse Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that he been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel prote to produce a sodium current into the transfected cell; (3) a method of
                                                                                                                                                                                                                         19-NOV-1998;
                                                                                                                                                                                                                                                         21-MAY-1999
                                                                                                                                                                                                                                                                                     FR2771103-A1
                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    neuropathic
                                                                                                                                                                                                                                                                                                                                                                                    diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Stabilised cDNA encoding type 5 sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60244 standard; cDNA;
                                                                                                                           Dietrich PS,
                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                          20-NOV-1997;
                                                                                                                                                                                                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128;
                                                                                                                                                                                                                                                                                                                                                                         root ganglia; tetrodotoxin; "TX; epiteps; stroce; ic neuropathy; traumatic injury; AIDS-related neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                  sodium channel; PN5; nervous system; plexiform;
root ganglia; tetrodotoxin; TTX; epilepsy; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                             DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                  pain; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                           Fish LM,
                                                                                                                                                                                          97US-0066225P
                                                                                                                                                                                                                         98FR-00014551
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71.1%;
                                                           sodium channel
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Pred. No. 8.4e-18;
0; Mismatches 51;
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70
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                                                              nervous
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                                                                                                                             Sangameswaran
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The present sequence encodes a type 5

sodium channel protein designated

Example

7; Fig 5A-E;

90pp; French.

epilephy, stroke, diabetic neuropathy, traumatic injuries, AIDS-related neuropathy, and especially neuropathic pain, e.g. migraine and headache PN5. The protein is a sodium ion channel of the nervous system, and is highly expressed in plexiform and dorsal root ganglia. The protein can be used to identify inhibitors of sodium channel proteins that are resistant to tetrodotoxin (TTX). The inhibitors are potentially useful for treating Length 5334;

ភិនិនិនិនិន្និនិ Query Match Best Local S Matches 83 Sequence 5334 BP; 1300 A; 1338 C; 1314 G; 1382 T; 0 U; 0 Other; 29.1%;

15 CANANTGACTTGGGAANACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 83; Similarity Conservative 0 Score 65; DB 2; Pred. No. 9.2e-11; 0; Mismatches 30 30; Indels 0; Gaps

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RESULT 15 ADD32209 ADD32209 standard; cDNA; 5298 ADD32209; В₽

Rat Na v 1.9 sodium channel protein encoding cDNA SEQ IJ

NO:19

15-JAN-2004

(first entry)

expression vector; Na v 1.9 sodium channel protein; sodium channel protein; dorsal root ganglion neuron; rat; gene; ss

The present invention describes an expression vector comprising a nucleic acid sequence that encodes a mammalian Na v 1.9 sodium channel protein or its fragment, and producing a sodium current when transfected in a cell. Also described: (1) a recombinant cell comprising the plasmid selected from prNaN, pCMV-rNaN-GFP, pLG338XM-rNaN and the plasmid described above; (2) a method of making a cell or cell line that produces a Na v 1.9 sodium channel-dependent sodium current by: (a) providing a cell that has been transfected with the expression vector; and (b) culturing the cell under conditions that allow expression of Na v 1.9 sodium channel protein

to produce a sodium current into the transfected cell; (3) a method of screening for an agent that modulates sodium current in a cell by: (a) exposing the cell or cell line produced by the method to the agent; and (b) measuring sodium current following exposure to the agent, where an alteration in the level of sodium current is indicative of an agent capable of modulating sodium current in a cell; and (4) a recombinant cell comprising the expression vector. The expression vectors are useful for the stable cloning and expression of the Na v 1.9 sodium channel at the mRNA and protein levels, and for producing sodium channel currents characteristic of native currents in dorsal root ganglion neurons. The present sequence encodes a rat Na v 1.9 sodium channel protein, which is used in the exemplification of the present invention.

Sequence 5298 BP; 1293 A; 1327 C; 1303 G; 1375 T; 0 U; 0 Other;

á Matches Query Match Best Local ( 15 75; Similarity CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT Conservative 26.1%; 72.8%; <u>.</u> Score 58.2; DB 9; Pred. No. 1.6e-08; 0; Mismatches 28 DB 9; 28; Length 5298; Indels 0, Gaps 74 0

밁 밁 S 5256 5196 CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTGCAATGGAGACTT 5255 75 GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGA 117 GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGA 5298

Search completed: March 22, Job time: 165.414 secs 2004, 16:13:24 THIS PAGE BLANK (USPTO)

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US07_NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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US-10-388-470-1
US-10-388-470-1
US-10-388-470-1
US-10-027-632-26965
US-09-885-478-3
US-09-889-732-3
US-09-899-732-3
US-10-341-751-3
US-10-027-632-135714
US-10-027-632-135715
US-10-027-632-26966
US-10-027-632-26966
US-10-160-758-6
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           Sequence 41, Appli
Sequence 1, Appli
Sequence 26965, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 135714,
Sequence 135715,
Sequence 135715,
Sequence 26966, A
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7, Appli
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Sequence 314,
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13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.3	13.3	13.3	13.3	13.3	13.4	13.4	13.4	13.4		13.5			13.5		13.5	13.5		13.5	13.5	13.5	13.5	13.6
594	594	594	594	594	594	594	613	613	591	434	434	20907	19929	2459	935	12425	12425	12425	12425	12425	1445	1336	1208	1208	1208	1208	1208	1208	174424
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US-10-158-790-10	42	US-10-141-761-10	US-10-140-472-10	US-10-146-731-10	US-10-123-155-10	US-10-142-426-10	US-10-027-632-4316	US-10-027-632-4315	US-10-027-632-292362	US-10-027-632-311468	US-10-027-632-311467	US-09-764-891-9966	US-09-764-891-9967	US-10-146-473-36	US-10-027-632-122142	US-10-616-187-50	US-10-023-523-50	US-10-023-529-50	US-10-671-242-50	US-09-976-740-50	US-09-945-527-6	US-10-102-806-247	US-10-616-187-16	US-10-023-523-16	US-10-023-529-16	US-10-671-242-16	US-09-976-740-16	US-09-962-055-16	US-09-960-706-969
Sequence 10, Appl	10,	10,	-	Sequence 10, Appl	10,		4316	4315		Seguence 311468,	311467	9966,	9967	Sequence 36, Appl	1221	50,	50,	50,	e 50,	50,	9	247,	16	16,	16,	Sequence 16, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 969, App

## ALIGNMENTS

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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR PILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
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US-10-388-470-41
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                                                                                Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dib-Hajj, APPLICANT: Waxman,
                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                          ENGTH: 5860
5295 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA 5353
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                                               CAAGGTGGACCAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA 64
                                                                                            Conservative
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                                                                                                               Score 200.6; DB 15; Pred. No. 1e-57;
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CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR PILING DATE: 1998-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-11-20
PRIOR PILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
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Sequence 4, Application US/10388470 Publication No. US20030228662A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dib-Hajj, Sulayman APPLICANT: Waxman, Stephen G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure LOCATION: (1996). (4042)
LOCATION: (1996). (4042)
OTHER INFORMATION: n = a or c or g or t. Xaa at amino acid position
OTHER INFORMATION: 652 is Leu; Xaa at amino acid position 1334 is Asn
OTHER INFORMATION: or Lys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (41)..(5335)
OTHER INFORMATION: cDN
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                                                                                                                                                                                                                                                                            GTCCAGCTTGGATGTGGCCAAGGTCAAGGTTCACAATGACTGAACCCTCATCTCCACCCC
                                                                                                                                                                                                                                                                                                                                                                               CAAACTGAGGCTGAAGGACAGGTCAAGTTCATCGCACCAGGTGTTTTTGCAATGGAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
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                                                                                                                                                                                                                                                                                                                              GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
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                                                                                                                                                                            TACCTCACTGCCTCACAGCTTAGCCTCCAGCCTCTGGCGAGCAGGCGGCAG 5406
                                                                                                                                                                                                                           TACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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74.3%;
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Sequence 26965, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus FEATURE: NAME/KEY: CDS LOCATION: (19)..(5313) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR EPILING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US99/02008 PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
LOCATION: (5804)
OTHER INFORMATION: cDNA sequence of mouse NaN, n = a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                               5266
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                              CTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAG 185
                                                                                                                                                                                                                                                                                        GGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTG-AGCCCTCAC 125
                                                                                                                                                                                                                                                                                                                                     AAGATGATCAAGCTGAAAGCTGAAAGGCAGGTCAAGTTCATCGCTCCAGGTGTTTTGCAAT
                                                                                                                                                                                                                                                                                                                                                                           AGGTGGACCAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAAT 66
                                                                                                                                                            CTGCACGCCTACCTCACAGCCTCACAGCTCAGCCCCCAGCCTCTGGCGAACAAGCGGCGG 5385
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71.1%;
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Pred. No. 6.2e-19;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-2

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; TYPE: DNA
; ORGANISM: RATTUS NORVEGICUS
US-09-885-478-3
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APPLICANT: LAZ, THOMAS M
APPLICANT: LAZ, THOMAS M
APPLICANT: NASISA
APPLICANT: NISON, AMY E
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 1795/57453-A-PCT-US
CURRENT PAPLICATION NUMBER: US/09/885,478
CURRENT PAPLICATION NUMBER: PCT/US99/31169
PRIOR APPLICATION NUMBER: PCT/US99/31169
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO
Sequence 3, Application US/09899732
Publication No. US20030082623A1
GENERAL INFORMATION:
APPLICANT: Salon et al, John A.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 1795/57453-C/JPW
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Best Local Similarity
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LENGTH: 639
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Best Local Similarity
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RESULT 8 US-10-029-314-3/c

Sequence 3, Application US/10029314
Publication No. US20030077701A1
GENERAL INFORMATION:

APPLICANT: Salon et al, John A

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US-10-341-751-3/c
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Publication No. US20040038855A1
GENERAL INFORMATION:
APPLICANT: Salon et al, John A.
TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof
FILE REFERENCE: 1795/57453-C/JPW
CURRENT APPLICATION NUMBER: US/10/341,751
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: 09/610,635
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 28
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LENGTH: 1214
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LENGTH: 1214
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CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/610,635
PRIOR FILING DATE: 2000-07-05
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ORGANISM: Rattus norvegicus
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                                  CCTCTGAGCTCCAGGGGTCA 184
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Pred. No. 0.69;
0; Mismatches 67;
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; TYPE: DNA; ORGANISM: Rattus norvegicus US-10-029-314-3
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US-10-027-632-135714
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SEQ ID NO 3
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Best Local Similarity
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SEQ ID NO 135714
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CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 09/899,732
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/610,635
PRIOR PILING DATE: 2000-07-05
PRIOR FILING DATE: 2000-07-05
NUMBER OF SEQ ID NOS: 28
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/185,218
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; Sequence 135715, Application US/10027632
; Publication No. US20030204075A9
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Best Local :
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                                                                  CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NT FILING DATE: 2002-04-30
APPLICATION NUMBER: US 60/218,006
FILING DATE: 2000-07-12
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                                                  FILING DATE: 2000-03-29
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APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
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; LENGTH: 732
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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US-09-970-944-3
                    RESULT 13
US-10-160-758-6/c
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PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 3
LENGTH: 14536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09970944 Publication No. US20030204052A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26966
Sequence
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Best Local
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APPLICANT: Rastelli, Luca
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids
TITLE OF INVENTION: Antibodies Directed Against these Proteins
FILE REFERENCE: 21402-13
CURRENT APPLICATION NUMBER: US/09/970,944
CURRENT FILING DATE: 2002-05-05
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-08-09
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                                                                                                ATACTTGATGGGCAGGCGTCTGCAGTGGAGGGAGGCAATGGCAG 14080
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Pred. No. 3.4;
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US-10-160-758-7/c
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                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/160,758
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
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CURRENT APPLICATION NUMBER: US/10/160,758
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
                                                                                                                                        Matches
                                                                                                                                                                                    Query Match
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TITLE OF INVENTION: CADS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EX02-089C
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                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                         Local Similarity
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Local Similarity 49.1%;
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    104 TCCACTGTGACTGAGCCCTCACCTCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCA 163
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Pred. No. 6.
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14184 ACATGTGTAGACATGTGCCCACATTGACCCTCCATGCATAGGGTTGAGTCGCTGCAGGTA 14125

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Qy 164 GCCTTCAGGGTCCAGGGGTTAGGGARAGGGAA 208

Db 14124 ATACTTGATGGGAGGGTCAGGAGGTATGGAAGGGAA 208

RESULT 15

US-09-967-768A-314/c

Sequence 314, Application US/09967768A

Patent NO. US20020150877A1

GENERAL INFORMATION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Sets

FILTE OF INVENTION: Sets

FILTE OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gancer Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gene Determination and Therapeutic Screening Using Signatu 1717LD OF INVENTION: Gene Determination and Therapeutic Screening Using Signatu 172

Db 1910R PILICATION NUMBER: US/69/967,768A

RESULT 15

RESULT 16

RESULT 1
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
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/cgn2_6/ptodata/2/pna/
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Copyright (c) 1993 - 2004 Compugen Ltd
/ cgn2_6/ptodata/2/pna/US06_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US08_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US08_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US081_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US081_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US083_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US083_COMB.seq:*
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/ cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
/ cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
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2/pna/PCTUS_CUMB.seq:*
--/HS06_COMB.seq:*
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466 / cgn1 6/ptodata/2/pna/US101B COMB seq:
467 / cgn2 6/ptodata/2/pna/US101B COMB seq:
488 / cgn2 6/ptodata/2/pna/US101B COMB seq:
489 / cgn2 6/ptodata/2/pna/US101B COMB seq:
590 / cgn2 6/ptodata/2/pna/US101B COMB seq:
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599 / cgn2 6/ptodata/2/pna/US101B COMB seq:
590 / cgn2 6/ptodata/2/pna/US101B COMB seq:
591 / cgn2 6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-646-224A-17

Sequence 17, Application US/09646224A
GENERAL INFORMATION:
APPLICANT: Glaxo Wellcome PLC
APPLICANT: Tate, Simon N
APPLICANT: Hicks, Caroline A
TITLE OF INVENTION: Ion Channels
FILE REFERENCE: PG3432
CURRENT APPLICATION NUMBER: US/09/646,224A
CURRENT APPLICATION NUMBER: GB 9805793.8
PRIOR APPLICATION NUMBER: GB 9805793.8
PRIOR APPLICATION OF SEQ 1D NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 17
LENGTH: 223
TYPE: DNA
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3 US-09-821-837-6884
9 US-09-997-022-3998
3 US-09-808-383-5398
3 US-09-808-383-5398
2 US-60-160-190-775
2 US-60-169-841-628
2 US-60-169-841-1341
1 PCT-US00-1934-41
3 US-09-813-846-412-84151
3 US-09-813-847-10-251
5 US-09-821-837-6819
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105-09-821-837-10-3471
105-09-825-550-1
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5 US-60-485-101-5
US-09-195-851-1
US-60-126-221-97
US-10-170-235-13985
2 US-60-453-050-33594
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                                                                                                                                                                                                                                                     Sequence 41, Appli
Sequence 3, Appli
Sequence 31, Appli
Sequence 317, App
Sequence 317, App
Sequence 8195, App
Sequence 8195, App
Sequence 11, App
Sequence 251, App
Sequence 111, App
Sequence 112304, Ap
Sequence 11304, Ap
Sequence 11304, Ap
Sequence 11, Appli
Sequence 1, Appli
Sequence 37, Appli
Sequence 1, Appli
Sequence 37, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Appl
Sequence 6884, Ap
Sequence 5398, Ap
Sequence 5398, Ap
Sequence 775, App
Sequence 628, App
Sequence 628, App
Sequence 1341, Ap
Sequence 155, App
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Sequence 6884, Application US/09821837

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2076-001
CURRENT APPLICATION NUMBER: US/09/821,837
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/193,481
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 9928
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6884
LENGTH: 532
                                                                                                       RESULT 3
US-09-397-022-5398
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US-09-821-837-6884
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US-09-646-224A-17
Sequence 5398, Application US/09397022
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 223; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 CCAAGGTGACCAAAATGACTT-GGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA
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                                                                                                                                                                                                                                  GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 223
                                                                                                                                                                                                                                                                                                                           CCTCCACGCCTACCTCATAGCCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCA
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                                                                                                                                                                                                        GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 483
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Pred. No. 2.1e-50;
0; Mismatches 4
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RESULT 4
US-09-808-383-5398
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; LENGTH: |555
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-808-383-5398
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; ORGANISM: Homo sapiens
US-09-397-022-5398
                                                      SOFTWARE: Fast. SEQ ID NO 5398
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PRIOR APPLICATION NUMBER: 60/107,257
PRIOR APPLICATION NUMBER: 60/126,906
PRIOR APPLICATION NUMBER: 60/126,906
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
NUMBER: OF SEQ ID NOS: 5775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5398, Application US/09808383 GENERAL INFORMATION:
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SEQ ID NO 5398
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/397,022
CURRENT FILING DATE: 199-09-15
PRIOR APPLICATION NUMBER: 60/100,465
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/106,443
                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/106,443
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: US 60/107,257
PRIOR FILING DATE: 1998-11-15
PRIOR APPLICATION NUMBER: US 60/126,906
PRIOR FILING DATE: 1999-03-30
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 99/397,022
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: US 60/100,465
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HOLTZMAN, DOUGLAS A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED
TITLE OF INVENTION: HUMAN FETAL SKIN LIBRARY
FILE REFERENCE: 1600.1046-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gearing, David P. APPLICANT: Holtzman, Dougle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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Local Similarity 97.7%;
hes 214; Conservative
                                                                                                     APPLICATION NUMBER: US 60/132,099
FILING DATE: 1999-04-30
R OF SEQ ID NOS: 5775
ARE: PastSEQ for Windows Version 4.0
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Pred. No. 2.1e-50;
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RESULT 6
US-60-160-190-775
US-60-160-190-775
; Sequence 775, Application US/60160190
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000115
; CURRENT APPLICATION UNMBER: US/60/160,190
; CURRENT FILING DATE: 1998-10-19
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; ORGANISM: HUMAN
US-60-160-190-1098
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US-60-160-190-1098
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GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN

TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000115
CURRENT APPLICATION NUMBER: US/60/160,190
CURRENT FILING DATE: 1998-10-19
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1098
LENGTH: 588
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Best Local Similarity
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Local Similarity 97.7%;
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97.7%;
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Pred. No. 2.1e-50;
0; Mismatches 4
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Pred. No. 2.1e-50;
0; Mismatches 4
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; LENGTH: 589
; TYPE: DNA
; ORGANISM: HUMAN
US-60-160-190-775
US-60-169-841-1341; Sequence 1341, Application; GENERAL INFORMATION:
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US-60-169-841-628
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL000163
CURRENT APPLICATION NUMBER: US/60/169,841
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 2910
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 628
LENGTH: 589
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Best Local Similarity 97.7
Matches 214; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 775
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Best Local Similarity
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-60-169-841-628
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                               CCTCCACGCCTACCTCATAGCTTCACAGCCTTGAGCCTTCTGAGCTCCAGGGGTCA 184
                                                                                                                                                                                                                                             ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCCAAGGTCCACTGTGACTCGAGCCCTCA 124
                                                                                                                                                                                                                                                                                      CAAGGTGGACCAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCA 64
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                   US/60169841
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                                                                                                                                                                                                                                                                                                                                                    Score 200.6; DB 7; Pred. No. 2.1e-50; 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                DB 72; Length
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; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHAN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REPERENCE: CL000163
; CURRENT APPLICATION NUMBER: US/60/169,841
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 2910
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1341
; ORGANISM: Human
US-60-169-841-1341
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Beasley, Ellen

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000703

CURRENT APPLICATION NUMBER: US/60/213,846

CURRENT FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 1617

SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0

SEQ ID NO 155

LENGTH: 972

TYPE: DNA

COGANISM: HUMAN

US-60-213-846-155
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Matches
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Best Local Similarity
Matches 214; Conserv
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hes 214; Conserv
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GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT
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97.7%; Pred. No. 2.1e-50;
tive 0; Mismatches 4
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PCT-US03-08611-3
; Sequence 3, Application PC/TUS0308611
; GENERAL INFORMATION:
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PCT-US00-19342-41
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                                                                                                                                APPLICANT: Transmolecular, Inc.
APPLICANT: GONDA, Matthew A
APPLICANT: GONDA, Matthew A
APPLICANT: GREENWOOD, John D
TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium Chanr
FILE REFERENCE: 51530-5007-WO
CURRENT APPLICATION NUMBER: PCT/US03/08611
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US 60/365,550
PRIOR PLING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO
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Best Local Similarity
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FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION:
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APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (31)...(5403)
OTHER INFORMATION: full length cDNA sequence for human NaN
                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                ENGTH: 5860
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Pred. No. 3.9e-50;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)...(5403)
; OTHER INFORMATION: full length cDNA sequence for human NaN
US-10-388-470-41
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US-10-388-470-41
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Best Local Similarity
Matches 214; Conserv
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TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/10/388,470
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: US/09/354,147C
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1999-01-29
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5474
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  GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 5512
                                                                                                                                 CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCA 184
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                           GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT
                                                                                     CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCA
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Pred. No. 3.9e-50;
0; Mismatches 4;
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Pred. No. 3.9e-50;
0; Mismatches 4
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US-60-516-609-317; Sequence 317, Application US/60516609; GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Transmolecular, Inc.

APPLICANT: GONDA, Matthew A

APPLICANT: GREENWOOD, John D

APPLICANT: DIB-HANAJ, Sulayman D
                                                         APPLICANT: Oncotech. Inc.
APPLICANT: Fruehauf, John P.
APPLICANT: Fruehauf, John P.
APPLICANT: Petka, Michael
TITLE OF INVENTION: Methods for Identifying and Classifying Tumor Samples
TITLE OF INVENTION: Uncertain Etiology
FILE REFERENCE: MBHB 03-24
CURRENT APPLICATION NUMBER: US/60/516,609
CURRENT FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 1065
SOFTWARE: PatentIn version 3.2
SEQ ID NO 317
LENGTH: 6237
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NAME/KEY: CDS
LOCATION: (31)..(5403)
OTHER INFORMATION:
S-60-365-550-3
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SEQ ID NO 3
LENGTH: 5860
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PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/072,990
PRIOR APPLICATION NUMBER: 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR FILING DATE: 1998-01-29
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TITLE OF INVENTION: Recombinant Expression Vectors
FILE REFERENCE: 51530-5007-PR
CURRENT APPLICATION NUMBER: US/60/365,550
CURRENT FILING DATE: 2002-03-20
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PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 21
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ORGANISM: Homo
                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Sequence 8399, Application US/09770175
(GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ANITITLE OF INVENTION: THEREFOR
TITLE DOF INVENTION: THEREFOR
CURRENT APPLICATION NUMBER: US/09/770,175
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,874
PRIOR FILING DATE: 2000-01-28
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US-60-516-609-317
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; ORGANISM: Homo sapiens
US-09-770-175-8399
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US-09-770-175-8399
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8399
LENGTH: 6499
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                                              CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGGTCA 5639
                                                                   CCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCA 184
                                                                                                                       ATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCA
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Pred. No. 4e-50;
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Search completed: March 23, Job time: 1689.54 secs

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| (cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-10-767-701-6510
US-10-796-280-11234
US-60-548-091-5682
US-10-796-280-112414
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US-10-100-683-3394
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Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
7470, 1	12393,	10851,	3836, Ap	30, App	6322, Ap	21553, 1	12230, A	10843, A	24, App1	14214, A	124, App	73, Appl	5600, Ar	5680, Ap	10845, A	927, App	3366, Ap

## ALIGNMENTS

RESULT 1 US-60-545-213-2723

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              Sequence 2724, Application US/60545213
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: TITLE OF INVENTION: Target Genes
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SEQ ID NO 2723
LENGTH: 1400
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Best Local Similarity
Matches 213; Conserv
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APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
NUMBER OF SEQ ID NOS: 303284
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REFERENCE: AM101083 (031896-042099)
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Pred. No. 3.3e-59;
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; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 6995
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity
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CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2724
LENGTH: 1400
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                                      GCAGCTTAGTGTATCAACAGGGAGTGGATTCACCAAATT 223
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Pred. No. 3.3e-59;
""" "" "" amatches 5; Indels
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US-60-545-213-6996

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; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6996

; LENGTH: 1400

; TYPE: DNA

; ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CCURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
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                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(1057)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Sorghum bicolor
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132 GCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCT 190
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Similarity 53.8%;
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                                                                                                               CTTGTCTAGCTTTGGGGTGGCCAAGGCCAAGGTCCACTGTGACTGAGCCCTCACCTCCAC 131
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97.3%;
                                                                                                                                                          Score 31; DB 6; Length 1057; Pred. No. 0.52; O; Mismatches 55; Indels
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Pred. No. 3.3e-59;
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: STENOSIS, METHODS OF DE
FILE REFERENCE: CL001510
CURRENT APPLICATION NUMBER: US/10/796,280
CURRENT FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 68533
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12234
                                                                                              RESULT 8 |
US-10-796-280-12414
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; ORGANISM: Homo sapiens
US-60-548-091-5682
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; Sequence | 5682, Application US/60548091
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Best Local Similarity 62.7
Marches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILE REFERENCE: CL001506

CURRENT APPLICATION NUMBER: US/60/548,091

CURRENT FILING DATE: 2004-02-27

NUMBER OF SEQ ID NOS: 24433

SOFTWARE: FRATSEQ for Windows Version 4.0

SEQ ID NO 5682

LENGTH: 21142
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APPLICANT: CARGILL, Michele et al.
Sequence 12414, Application US/10796280
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: D
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                                                                                                                                                                                                                168 CTGAGCTCCAGGGTCAGCAGCTTAGTGTATCAAC 202
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                                                                                                                                                                                                                                                                                         .08 CTGTGACTGAGCCCTCACCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTCAGCCT 167
                                                                                                                                                                                                                                                                                                                               54; Conservative
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                                                                                                                                                                                                                                                                                                                                                 Score 29.4; DI
Pred. No. 6.4;
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AND USES THEREOF
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; ORGANISM: Homo sapiens
US-60-545-213-4092
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US-60-545-213-4092
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                                      APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TILE REFERENCE: AM101083 (031896-042099)
CURRENT FILICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 30284
SOFTWARE: Patentin version 3.2
SEQ ID NO 4092
LENGTH: 600
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12414
LENGTH: 25930
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GENERAL INFORMATION:
APPLICANT: David W. Morris
                                                                                                                                                                                                                                                                                       Sequence 4092, Application US/60545213 GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOPTWARE: FASTSEQ for Windows Version 4.0
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TITLE OF INVENTION: Novel Therapeutic Targets
FILE REFERENCE: 529452001600
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les 62; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
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Pred. No. 9.6;
0; Mismatches 5
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RESULT 11
US-60-545-213-8364
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US-10-100-683-3370
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; LENGTH: 600
; TYPE: DNA
; CRGANISM: Homo sapiens
US-60-545-213-8364
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3370, Appli
GENERAL INFORMATION:
APPLICANT: Rosen, e
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target General Structure of Tructure of Invention: Target General AMI01083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3
                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                        APPLICATION NUMBER: US 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,845
FILING DATE: 1997-08-22
                                                      APPLICATION NUMBER: US 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
                                                                                                                                 APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: US 60/047,599
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/043,576 FILING DATE: 1997-04-11
                                                                                                                   FILING DATE: 1997-05-23
                                      FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632 FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3370
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TYPE: DNA
ORGANISM: Homo sapiens
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FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,601
FILING DATE: 1997-05-23
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APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
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APPLICATION NUMBER: US 60/040,162
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APPLICATION NUMBER: US 60/056,664
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PRIOR FILING DATE: 1997-08-22
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                                      CTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGG
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CCTCAGGACTGCACCTTAGGGCAGTGTCCGTCAGTG
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Pred. No. 3
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GGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTCATAG 144 Human Secreted Proteins Score 28.8; DE Pred. No. 3.5; 0; Mismatches See File Wrapper or PALM DB 6; 42; Length 1514; Indels 0

Gaps

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988

RESULT 14 US-10-100-683-13346/c ; Sequence 13346, Application US/10100683

GENERAL INFORMATION:

APPLICANT: Rosen, et al. TITLE OF INVENTION: Human Secreted Proteins

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Sequence 271, Application US/10775920

GENERAL INFORMATION:
APPLICANT: Mergen Ltd
FITLE OF INVENTION: POLYNUCLECTIDE SEQUENCES AND CORRESPONDING ENCODED POLYDEPTIDES
TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
TITLE OF INVENTION: IN CERTAIN CANCERS
FILE REFERENCE: Mergen - 0010B
CURRENT APPLICATION NUMBER: US/10/775,920
CURRENT PILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/447,900
PRIOR APPLICATION NUMBER: US 60/447,900
PRIOR PILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 385
SOFTWARE: PRATE 2003-03.2
SEQ ID NO 271
LENGTH: 4132
TYPE: DNA
ORGANISM: Homo sapiens
US-10-775-920-271
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NUMBER OF SEQ ID NOS: 13468
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13346
LENGTH: 4628
TYPE: DNA
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/440,162
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
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APPLICATION NUMBER: US 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
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APPLICATION NUMBER: US 60/056,845
FILING DATE: 1997-08-22
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APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
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                                                           JOURNAL
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VERSION
KEYWORDS
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AY404475
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DEFINITION
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ORGANISM
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    TITLE
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4614)

Clark, A.G., Glanowski, S.; Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                  GSS.
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                                                                                       Science 302 (5652), 1960-1963 (2003)
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Homo sapiens
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BI417342
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BU048840
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BU785965
BB638780
BB74176
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BI915983
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AQ458796
AQ480354
BB541268
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AV561225 AV561225
CF948308 UI-D-GC1-CC517185 CH240_363
AL399697 T3 end of AL1066983 Drosophil
BI417342 LiNEST388
BU048840 PP_LE8003
BU785965 in48d05.y
BB638780 BB638780
CG317804 OGXPP57TH
BH874175 hp48h11.g
BH771086 603059656
CC422910 PUHFJ04TD
BE230112 99AS344 R
BC2422910 PUHFJ04TD
BE230112 99AS344 R
BC2422910 PUHFJ04TD
BE23012 99AS344 R
BC242056 CH240_230
BU265240 603817637
CB736496 AMGNNUC:N
BU915983 603177095
AK086309 MU8 muscu
BB196236 BB196236
BB065876 BB065876
AQ830694 HS 5563 A
AI632307 tc22d06.x
BU916339 N063D12 P
BM54468 AGENCOURT
AI198288 AGENCOURT
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AGGTGGACCAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAAT 66
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                                   Conservative
                                                                                                                                                                                                                                                                                         sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                     /gene="SCN11A"
/locus_tag="HCM1903"
                                                                                                                                                                                                                                                    Location/Qualifiers
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/mol_type="genomic DNA"
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Pred. No. 2.6e-16;
0; Mismatches 4
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TRANSCRIPT, partial sequence,
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BX673737 723 bp m
BX673737 Sus Scrofa library (scac) S
scac0040i.a.14 5prim, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10873.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDMA libraries and normalization Unpublished (2001)
On Feb 16, 2001 this sequence version replaced Contact: Genoscope
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                                                                                                                                                                                    CCTTGCCTTCAGCCTCTGAGCTCC 176
                                                                                                                                                                                                                                                                   CAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTCATAGCTTCACAG 152
                                                                                                                                                                                                                                                                                                              CGGNSCGMHTVTCCSAGGGCTGACTCTSCSSTGGGAMWSSGCTTGTCGCTVTGSGSKGGG 909
                                                                                                                                                                                                                                                                                                                                                      CGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTTGTCTAGCTTTGGGGGTGGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGATGATCAAGCTGAAAGCTGAAAGGCAGGTCAAGTTCATCGCTCCAGGTGTTTTGCAAT 4505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="CS0DI023YC04"
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                                                                                                                                                                                                                                                                                                                                                                                                             16.1%; Score 35.8;
39.6%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                 27;
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                       Sus
                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                 60;
                       scrota
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RESULT 5
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Best Local S
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                                                                              ORGANISM
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  AUTHORS
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BX673737.1
EST.
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AQ848329.1
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Soares, M., Bonaldo, F. and Hatey, F. A Pig Normalised Multi-Tissue cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
                                                                                                                                                                                              LMAJFV1_lm60d08.x1 Leishmania major
Leishmania major genomic clone LMAJF
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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1 (bases 1 to 521)
Akopyants, N.S., Clifton, S.W.,
                                                       Eukaryota; Euglenozoa;
                                                                              Leishmania
                                                                                               Leishmania major
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                                       Leishmania
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/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scac)"
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58.1%;
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kref="-
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O; Mismatches
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                                                         Kinetoplastida; Trypanosomatidae;
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Martin, J.,
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major FV1 random genomic library
LMAJFV1_lm60d08 3', genomic survey
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Pape, D., Wylie, T., Li, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Washington University Genome Sequencing Center If using this information please cite:

N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major Friedlin strain V1 genome by shotgun sequencing' and the Washington University Genome Sequencing Center For information on obtaining Clone material please contact: Natalia S. Akopyants Ph.D. (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D. (beverley@borcim.wustl.edu)
                                                 genomic survey sequence CE037831
                                                                                          tigr-gss-dog-17000349541289
                                                                                                                     CE037831
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A survey of the Leishmania major Friedlin strain V1
shotgun sequencing: a resource for DNA microarrays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
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                                                                                                                                                                                                                                                                                                                                                                      CACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCTTAGTGTATCAACAGGGA 207
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                                                                                                                                                                                                                                                                                  GTGGATTCACCAAATT 223
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Location/Qualifiers
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/mol type="genomic DNA"
/mol type="genomic DNA"
/strain="Friedlin strain V1"
/strain="Friedlin strain V1"
/db xref="Taxon:5664"
/clone="LMAJFV1 lm60d08"
/lab host="TOP10 (Invitrogen)"
/clone lib="Leishmania major FV1 random genomic library"
/clone lib-"Leishmania major FV1 random genomic library"
/note="Vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
polymerase, dephosphorylated with Shrimp Alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphatase and ligated into pZero-2 vector's EcoRV site."
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dd 9
                                                                                               Library Canis familiaris
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SOURCE

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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (Dases 1 to 576)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                              Ostreococcus tauri
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales;
Mamiellaceae; Ostreococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                Derelle,E., Ferraz,C., Lagoda,P., Eychenie,S., Sabau,X., Courties,C., Delseny,M., Demaille,J.,
                                             Seq primer: forward
                                                                                                               BP 44,
                                                                                                                                   CNRS UMR 7628
                                                                                                                                                                Contact: Moreau
                                                                                                                                                                                  J. Phycol. 38 (6), 1150-1156
                                                                                                                                                                                                                                   DNA libraries for sequencing the genome of Ostreococcus tauri
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                                                              Email: h.moreau@obs-banyuls.fr
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                                                                              (33) 468887309 (33) 468887398
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
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/mol_type="genomic DNA"
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/strain="Standard Poodle"
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Email: asamizu@kazusa.or.jp,
Location/Qualifiers
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/clone="ota21e06.b"
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/mol_type="genomic DNA"
/strain="OTTH0595"
                                                                                                               tissue_type="green siliques"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                organism="Arabidopsis"
|mol_type="mRNA"
                                                                                                                                                                             clone="SQ232e07F"
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                                                                                                                                                                                                                  strain="Columbia"
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URL:http://www.kazusa.or.jp/en/plant/.
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EST.
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Kazusa DNA Research Institute
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  TCTTTGGCGNCGATCCAACGACTTCTCATCTCCACGTACGAGAAGCTCTTCCTCTGATCA
                                           GCTTCACAGCCTTGCCTTCAGCCTCTGAGCTCCAGGGGTCAGCAGCTTAGTGTATCAACA 203
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                                                                                                                                             TGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCCTACCTCATA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 571)
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="$Q147g09F"
/tlssue_type="green siliques"
/clone_lib="hxrabidopsis thaliana green siliques (
/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                             15.2%;
48.9%;
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                                                                                                                                                                                                                                                                                        Score 33.8; D)
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana: Generation sequence tags from normalized and
                                                                                                                                                                                                                                                                                                                                           BG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Columbia"
; Site_2:
                                                                                                465
  525
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AUTHORS
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CF948308/c
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PUBMED
Query Match 15...
Best Local Similarity 53...
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CF948308 1inear EST 1 UI-D-GC1-aag-o-07-0-UI.sl UI-D-GC1 Alexandrium tamarense UI-D-GC1-aag-o-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/dinoflagellate.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alexandrium tamarense Alexandrium tamarense
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu
Tissue Procurement: Provasoli-Guillard National Center for Culture
of Marine Phytoplankton (CCMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 632)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Dinophyceae; Gonyaulacales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF948308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13 FORWARD
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                                                                                                                                                                                        /note="Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1 ECOR I; Site_2: Not I; UI-D-GC1 is a normalized library derived from UI-D-GC0. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TACCTCGAGA. Tissue was obtained from the Provasoli-Guillard National Center for Culture of Marine Phytoplankton (CCNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UI-D-GC1-aag-o-07-0-UI"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-D-GC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="CCMP 1598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Alexandrium tamarense"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:2926"
                      15.2%;
                                                                                                                                                                    TISSUE=Alexandrium tanarense
  0,
                         Score 33.8;
Pred. No. 53
  Mismatches
                           53;
                                                  DB 14;
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                                                  Length 632;
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CC517185/c
                                                                                                             ORIGIN
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  Query Match
Best Local S
Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                               source
  Local Similarity 58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC517185 796 bp CC517187 363120.T7 CHORI-240 Bos ti genomīc survey sequence.
CC517185 CC517185.1 GI:31835473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TBai,M., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., TBai,M., Cloutier,A., Lee,D., Girn,N., Cloun,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Glon,R., Chan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W., Dalrymple,B.P. and Tellam,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T7
Class: BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Other_GSSs: CH240_363I20.TARBAC13P2
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC ends.
                                                                                                                             /cell_type="Blood"
/clone_lib="CHORI-240"
/clone_tib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford_bull_Li_Domino_99375; CHORI-240_Bovine_BAC
library (Male) produced_by_Pieter_de_Jong"
                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                     organism="Bos taurus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                         clone="CH240_363I20"
                                                                                                                                                                                                                                                                                                                    db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                             strain="breed: Hereford"
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                        15.0%;
  Pred. No. 79;
D; Mismatches
                                                      Score 33.4;
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                                                      DB 29; Length 796;
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     41;
     Indels
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AUTHORS
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MEDLINE
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CNS06IOR
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                   /note="end : T3"
/note="end : T3"
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/note="similar to Saccharomyces cerevisiae ORF YPR160w [
                                                                                                                                                           /db_xref="taxon:4931"
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/clone_lib="ASOAA"
                                                                                                                                                                                                                                                                /organism="Saccharomyces
/mol_type="genomic DNA"
/strain="CLIB 533"
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                                                                                                                                     exiguus, Saccharomyces sérvazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                               Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequef@genoscope.cns.fr - Web: www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Souciet, J.L., Algle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Algle, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Ge-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
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AL398194.1 GI:12151485
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Aigle, M. and Durrens, P
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                    /mol_type="genomic DNA"
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Pred. No. 86;
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Query Match
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                                                                                                                                                                                                                                                             Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ososgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CAAAATGACTTGGGAAAACGGGCCTCATTCACCACTCCAGACTCTTTGCAATGGAGACTT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS007C8 1001 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR15M24 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL066983.1 GI:4945547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGATGTCTGGGCAACAAATGGCCGAATAAGCCAACGGGCCATTTTTTCCAAGGCTTCTT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATAACGGTGTGGTTGGTGAAGCAAAGGTCTTGGTGACAATGTCCCAAGCTTCGTGCC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTAGCTTTGGGGTGGCCAAGGGCAAGGTCCACTGTGACTGAGCCCTCACCTCCACGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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   GPH1 ; glycogen phosphorylase }
   putative frameshift(s)"
                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mb.type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR15M24"
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/note="end : T3"
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                                                                                                                            clone_lib="RPCI-98"
     15.0%;
37.8%;
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  Score 33.4;
Pred. No. 89;
                                                                                                       TET3"
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Pred. No. 89
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                            DB 29;
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                            Length 1001;
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REFERENCE
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VERSION
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                                       163
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                                                                              126
                                                                                                                 103 GTCCACTGTGACTGAGCCTCACCTCCACGCCTACCTCATAGCTTCACAGCCTTGCCTTC 162
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  99
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                                                                                                                                                                                                                                      68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI417342
459 bp mRNA linear EST 15-AUG-2001 L/NEST38a9r Lotus japonicus nodule library 5 and 7 week-old Lotus corniculatus var. japonicus cDNA 5', mRNA sequence.
BI417342
BI417342.1 GI:15188365
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lotus japonicus root nodule ESTs: tools for functional genomics Unpublished (2000)
Contact: Udvardi MK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: udvardi@mpimp-golm.mpg.de
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Busaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                     AGCCTC 168
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                                                                              TTCCGCTTTGTCTTCTCCGTCACGTACGCCACCAGCTCCTTTGCGTCCATCGTCCCCTTC
                                                                                                                                                        TCACCACCTCCTTTCTTTCTTATCTTCTTTCTTTGTTGGTGGGACCACCATCCACG 127
                                                                                                                                                                                           TCACCACTCCAGACTCTTTGCAATGGAGACTTGTCTAGCTTTGGGGTGGCCAAGGGCAAG 102
ACCGTC 61
                                                                                                                                                                                                                                      Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                /note="Organ: Nodule; Vector: pSPORT1; Site_1: Sall; Site_2: Notl; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lotus corniculatus var. japonicus"
/mol type="mRNA"
/mol type="mRNA"
/culTivar="Gifu (B-129)"
/culTivar="Gifu (B-129)"
/db xref="taxon:34305"
/dev stage="5 and 7 week-old plants"
/clone_lib="Lotus japonicus nodule library 5 and 7
                                                                                                                                                                                                                                                      14.9%;
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                                                                                                                                                                                                                                  Score 33.2; DE Pred. No. 67; 0; Mismatches
                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                      58;
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